

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 06:11:33 ; Search time 51 Seconds

(without alignments)
78.173 Million cell updates/sec

Title: US-09-548-449-8

Perfect score: 13

Sequence: 1 aatcaannanta 13

Scoring table: IDENTITY_NUC

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCMTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	76.9	29	4	US-09-593-012-112
2	10	76.9	36	2	US-08-669-721-1
3	10	76.9	36	2	US-08-669-721-1
4	10	76.9	36	4	US-09-189-344-1
5	10	76.9	36	4	US-09-189-344-1
6	10	76.9	96	6	5190931-4
7	10	76.9	100	1	US-08-145-705A-17
8	9.2	70.8	72	1	US-07-737-071A-3
9	9.2	70.8	72	1	US-08-022-096-3
10	9	69.2	15	1	US-08-334-847-467
11	9	69.2	17	3	US-08-985-162-812
12	9	69.2	17	3	US-08-985-162-812
13	9	69.2	17	3	US-08-985-162-812
14	9	69.2	18	4	US-09-241-581B-2
15	9	69.2	18	4	US-08-265-428-2
16	9	69.2	18	5	PCT-US95-07721-2
17	9	69.2	20	2	US-08-743-637B-39
18	9	69.2	20	3	US-08-526-840B-39
19	9	69.2	20	3	US-08-680-506-18
20	9	69.2	20	3	US-09-357-073-43
21	9	69.2	20	3	US-09-288-461-20
22	9	69.2	20	4	US-09-889-595-17
23	9	69.2	21	1	US-08-328-961-12
24	9	69.2	21	1	US-08-462-397-12
25	9	69.2	21	2	US-08-468-819-30
26	9	69.2	21	2	US-08-468-819-30
27	9	69.2	22	2	US-08-613-417A-25

28	9	69.2	22	3	US-08-594-452-25	Sequence 25, Appl
29	9	69.2	22	3	US-08-578-686C-24	Sequence 24, Appl
30	9	69.2	22	3	US-08-281-203-18	Sequence 18, Appl
31	9	69.2	22	3	US-09-094-405-29	Sequence 29, Appl
32	9	69.2	22	3	US-09-258-408-25	Sequence 25, Appl
33	9	69.2	22	3	US-09-196-132-25	Sequence 25, Appl
34	9	69.2	22	3	US-09-144-112-24	Sequence 24, Appl
35	9	69.2	22	4	US-08-337-120A-33	Sequence 33, Appl
36	9	69.2	24	1	US-07-722-798A-74	Sequence 74, Appl
37	9	69.2	24	4	US-09-561-825-12	Sequence 12, Appl
38	9	69.2	24	4	US-09-514-302-10	Sequence 10, Appl
39	9	69.2	26	1	US-07-722-798A-73	Sequence 73, Appl
40	9	69.2	26	3	US-08-594-452-97	Sequence 97, Appl
41	9	69.2	26	3	US-08-594-452-98	Sequence 98, Appl
42	9	69.2	26	3	US-09-258-408-97	Sequence 97, Appl
43	9	69.2	26	3	US-09-258-408-98	Sequence 98, Appl
44	9	69.2	29	4	US-09-302-620B-8	Sequence 8, Appl
45	9	69.2	30	1	US-08-460-784-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-593-012-112/c
Sequence 112, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTE
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 112
LENGTH: 29
TYPE: DNA
ORGANISM: Paecilomyces variotii
US-09-593-012-112

Query Match 76.9%; Score 10; DB 4; Length 29;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AATCAANNANTA 13
Db 27 AATCAATCAATTA 15

RESULT 2
US-08-669-721-1
Sequence 1, Application US/08669721
Patent No. 5834236
GENERAL INFORMATION:
APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,721
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REFERENCE/DOCKET NUMBER: 07251/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-669-721-1

Query Match 76.9%; Score 10; DB 2; Length 36;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTTA 13
||||| |
DB 9 AATCAATTAATTA 21

RESULT 3
US-08-669-721-1/c
Sequence 1, Application US/08669721
Patent No. 5834236
GENERAL INFORMATION:
APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: LA JOLLA
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,721
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REFERENCE/DOCKET NUMBER: 07251/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-669-721-1

Query Match 76.9%; Score 10; DB 2; Length 36;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNNTTA 13
||||| |
DB 32 AATCAATTAATTA 20

RESULT 4
US-09-189-344-1
Sequence 1, Application US/09189344
Patent No. 6191258
GENERAL INFORMATION:
APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: LA JOLLA
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,344
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/669,721
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REFERENCE/DOCKET NUMBER: 07251/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-189-344-1

Query Match 76.9%; Score 10; DB 4; Length 36;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTTA 13
||||| |
DB 9 AATCAATTAATTA 21

RESULT 5
US-09-189-344-1/c
Sequence 1, Application US/09189344
Patent No. 6191258
GENERAL INFORMATION:
APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: LA JOLLA
STATE: CA

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; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/669,721
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-189-344-1
;
Query Match          76.9%; Score 10; DB 4; Length 36;
Best Local Similarity 76.9%; Pred. NO. 1.5e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 AATCAANNANTTA 13
Db 32 AATCAATTAATTA 20
;
RESULT 6
5190931-4
; Patent No. 5190931
; APPLICANT: INOUE, MASAYORI
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION BY
; EMPLOYING TRANSLATIONAL INHIBITION OF mRNA UTILIZING
; INTERFERING COMPLEMENTARY RNA
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/436,598
; FILING DATE: 15-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 300,741
; FILING DATE: 23-JAN-1989
; APPLICATION NUMBER: 228,852
; FILING DATE: 03-AUG-1988
; APPLICATION NUMBER: 543,528
; FILING DATE: 20-OCT-1983
; SEQ ID NO:4:
; LENGTH: 96
;
5190931-4
;
Query Match          76.9%; Score 10; DB 6; Length 96;
Best Local Similarity 76.9%; Pred. NO. 1.5e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 AATCAANNANTTA 13
Db 42 AATCAATTAATTA 54
;
RESULT 7
US-08-145-705A-17/C
; Sequence 17, Application US/08145705A
; Patent No. 5489513

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; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang, Plempel, Manfred;
; APPLICANT: L Dberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; City: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC Powermate 1 plus
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
;
US-08-145-705A-17
;
Query Match          76.9%; Score 10; DB 1; Length 100;
Best Local Similarity 76.9%; Pred. NO. 1.5e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 AATCAANNANTTA 13
Db 56 AATCAATTAATTA 44
;
RESULT 8
US-07-737-071A-3/C
; Sequence 3, Application US/07737071A
; Patent No. 529286
; GENERAL INFORMATION:
; APPLICANT: JARSCH, Michael
; APPLICANT: LANG, Gunter
; TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
; TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC
; TITLE OF INVENTION: DEXTRANSICUS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Nikolaio, Marmelstein Kubovcik &
; ADDRESSEE: Murray
; STREET: 1725 K Street, N.W., Suite 1000
; City: Washington D.C.

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1 COUNTRY: United States of America
2 ZIP: 20006
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patentin Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/07/737,071A
11 FILING DATE: 19910730
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: DE P 4024158.9
15 FILING DATE: 30-JUL-1990
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Murray, Robert B.
18 REGISTRATION NUMBER: 22,890
19 REFERENCE/DOCKET NUMBER: 911028
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (202) 659-2930
22 TELEFAX: (202) 887-0357
23 TELEX: 440142
24 INFORMATION FOR SEQ ID NO: 3:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 72 base pairs
27 TYPE: NUCLEIC ACID
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30
31 US-07-737-071A-3
32
33 Query Match 70.8%; Score 9.2; DB 1; Length 72;
34 Best Local Similarity 61.5%; Pred. No. 4.4e+03;
35 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0
36
37 QY 1 AATCAANNANTTA 13
38 ||||| |||
39 Db 51 AAYCAATATATTM 39
40
41 RESULT 9
42 US-08-022-096-3/C
43 Sequence 3, Application US/08022096
44 Patent No. 5308770
45
46 GENERAL INFORMATION:
47 APPLICANT: JARSCH, Michael
48 APPLICANT: LANG, Gunter
49 TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
50 TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC
51 TITLE OF INVENTION: DEXTRANICUS
52 NUMBER OF SEQUENCES: 5
53 CORRESPONDENCE ADDRESSES:
54 ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
55 STREET: 655 Fifteenth Street N.W. Suite 330
56 CITY: Washington
57 STATE: D.C.
58 COUNTRY: U.S.A.
59 ZIP: 20005-5701
60
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: Patentin Release #1.0, Version #1.25
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/022,096
68 FILING DATE: 19930225
69 CLASSIFICATION: 435
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: DE P 40 24 158.0
72 FILING DATE: 30-JUL-1990
73 PRIOR APPLICATION DATA:
74 APPLICATION NUMBER: US 07/737,071
75 FILING DATE: 30-JUL-1991
76 ATTORNEY/AGENT INFORMATION:

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NAME: Chin, Monica F.
REGISTRATION NUMBER: 36, 105
REFERENCE/DOCKET NUMBER: P564-3005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-08-022-096-3

Query Match 70.8%; Score 9.2; DB 1; Length 72;
Best Local Similarity 61.5%; Pred. No. 4.4e+03;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
||| ||| |||
Db 51 AATCAATTAATTTT 39

RESULT 40
US-08-334-847-467
Sequence 467, Application, US/08334847
Patent No. 5693532
GENERAL INFORMATION:
APPLICANT: MCSwigen, James
APPLICANT: Draper, Kenneth
APPLICANT: Payco, Paul
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334, 847
FILING DATE: No. 5693532member 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 467:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-334-847-467

Query Match 69.2%; Score 9; DB 1; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 ATCAANNANTTA 13
|:|:| | :|:
Db 2 AUCAAUAGUUA 13

RESULT 11
US-08-985-162-812/C

; Sequence 812, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 812:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-812

Query Match 69.2%; Score 9; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 AATCAANNANTT 12
|:|:| | |:
Db 16 AATCAAAATCTT 5

RESULT 12
US-08-985-162-813/C
; Sequence 813, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir

; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 813:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-813

Query Match 69.2%; Score 9; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 AATCAANNANTT 12
|:|:| | |:
Db 14 AATCAAAATCTT 3

RESULT 13
US-08-985-162-814/C
; Sequence 814, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 814:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-814

Query Match 69.2%; Score 9; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTT 12
||||| ||
DB 13 AATCAATACT 2

RESULT 14
US-09-241-581B-2
Sequence 2, Application US/09241581B
Patent No. 6350859
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8795
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et al.
JOURNAL: J. Lipid Res.
VOLUME: 34
PAGES: 983-1000
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 18
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-241-581B-2

Query Match 69.2%; Score 9; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTT 12
||||| ||
DB 1 AATCAAGAAAT 12

RESULT 15
US-08-265-428-2
Sequence 2, Application US/08265428
Patent No. 6429289
GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scavenger Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6558
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et al.
JOURNAL: J. Lipid Res.
VOLUME: 34
PAGES: 983-1000
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 18

US-08-265-428-2

Query Match 69.28; Score 9; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 5.9e+03;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCANNANTT 12
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 Db 1 AATCAGGAAAT 12

Search completed: December 26, 2002, 11:37:15
 Job time : 57 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 20:55:28 ; Search time 2628 Seconds

(without alignments)
5448.470 Million cell updates/sec

Title: US-09-548-449-3

Perfect score: 492
Sequence: 1 actcgcgcagcattcacc.....gccttaaccagcaagac 492Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_hla:*
2: gb_hla:*
3: gb_hla:*
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41: gb_hla:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	100.0	3761	1 PANR	X57736 P.aeruginos
2	492	100.0	3761	1 PSEANRPRO	M98276 Pseudomonas
3	490.4	99.7	11637	1 AE004582	X97961 P.aeruginos
4	281	57.1	2635	1 PAHEMN	X58405 P.aeruginos
5	90	18.3	900	1 PANR	AC087547 Oryza sat
6	51.8	10.5	129420	8 AC087547	AC087550 Oryza sat
7	49.8	10.1	175644	2 AP003771	AC090435 Chlamydom
8	49.4	10.0	68736	2 AC090435	AC090436 Chlamydom
9	49.4	10.0	102657	2 AC090436	AF061246 Ralstonia
10	49.2	10.0	3312	1 AF061246	AF033262 Pseudomon
11	48.2	9.8	2450	1 AF355797	AF355797 Homo sapi
12	48	9.8	2668	9 AC004678	AC004678 Homo sapi
13	48	9.8	38939	9 HSBRN3A2	U10063 Human POU d
14	47.8	9.7	13076	1 AE012233	AE012233 Xanthomon
15	47.6	9.7	40352	1 SC661A	AL352595 Streptomy
16	47.6	9.7	57078	2 AC125442	AP003232 Oryza sat
17	47.2	9.6	165497	8 AP003232	AP003232 Oryza sat
18	47.2	9.6	165497	8 AP003232	AP003232 Oryza sat
19	47.2	9.6	165497	8 AP003232	AP003232 Oryza sat
20	47	9.6	153180	2 AP004683	AP004683 Oryza sat
21	47	9.6	153180	2 AP004683	AP004683 Oryza sat
22	46.8	9.5	123580	1 AF263912	AF263912 Streptomy
23	46.8	9.5	125401	6 AX211739	AX211739 Sequence
24	46.8	9.5	134367	8 AP003842	AP003842 Oryza sat
25	46.8	9.5	169162	8 AP004267	AP004267 Oryza sat
26	46.4	9.4	42348	1 SC27611	AL391763 Streptomy
27	46.2	9.4	123071	2 AC121481	AC121481 Rattus no
28	46	9.3	2765	6 BD012188	BD012188 Novel can
29	46	9.3	2765	23 BD004868	BD004868 Novel can
30	46	9.3	3131	6 BD012187	BD012187 Novel can
31	46	9.3	3131	23 BD004867	BD004867 Novel can
32	46	9.3	3160	9 AB043584	AB043584 Homo sapi
33	46	9.3	3332	6 BD012186	BD012186 Novel can
34	46	9.3	3332	23 BD004866	BD004866 Novel can
35	46	9.3	3344	6 BD012182	BD012182 Novel can
36	46	9.3	3344	23 BD004862	BD004862 Novel can
37	46	9.3	3842	1 AF106004	AF106004 Streptomy
38	46	9.3	7603	9 HSA404614	AJ404614 Homo sapi
39	46	9.3	10206	1 AE012548	AE012548 Xanthomon
40	46	9.3	14478	1 SC2D4	AL392175 Streptomy
41	46	9.3	31624	1 SC4A7	AL161755 Streptomy
42	46	9.3	42526	2 AC098321	AL133423 Streptomy
43	46	9.3	58930	2 CNS05TEZ	AC098321 Rattus no
44	46	9.3	104782	9 CNS05TEZ	AL359681 Human chr
45	46	9.3	124539	2 AC044794	AC044794 Homo sapi

ALIGNMENTS

RESULT 1

PANR 3761 bp DNA linear BCT 18-NOV-1997

LOCUS P.aeruginosa anr gene for positive control element ANR.

DEFINITION X57736

ACCESSION X57736.1 GI:45359

VERSION anr gene: ANR protein; positive control element.

KEYWORDS Pseudomonas aeruginosa.

SOURCE Pseudomonas aeruginosa.

ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

REFERENCE 1 (bases 1 to 3761)

AUTHORS Zimmermann, A.

TITLE Direct Submission

JOURNAL Submitted (12-FEB-1991) A. Zimmermann, Institut f Mikrobiologie ETH

REMARK
REFERENCE
TITLE

2 (bases 1931 to 2958)
Zimmermann, A., Reilmann, C., Gailand, M. and Haas, D.
Anaerobic growth and cyanide synthesis of *Pseudomonas aeruginosa*
depend on *aur*, a regulatory gene homologous with *fur* of *Escherichia*
coli

JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Mol. Microbiol. 5 (6), 1483-1490 (1991)
92157874
1/87/798
3 (bases 1 to 3761)
Zimmermann, A.
Direct Submission
Submitted (25-FEB-1992) A. Zimmermann, same address
Location/Qualifiers
1. .3761
/organism="Pseudomonas aeruginosa"
/strain="PAO1"
/db.xref="taxon:287"
/map="60 min."
/clone_lib="pAER3"
22. .504
/note="ORF A"
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/db.xref="GI:45360"
/transl="MLDTRMDADLIRPYDLGSGRYTSYPAYQFHGIGFQDLHAL
RDSKRAKPLSLVYHPIPCANICCYCAKNVITTDGRSAPYLARLVREIVSRHLS
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CDS

564. .1061
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/transl="MPQRINADLPSPGKLEMLQTTTEOLAAGRYIGMDHFAFLP
DDELASAOEDGTLOKRNFGYTTGHGDLGVGSAISQIGLYSONSDINIDYOTSLD
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SPPA"

CDS

complement(1235. .1702)
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1948. .2682
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/transl="MAETIKVRLPQAHCKDCSLAPLCLPLSTVEDMDSIDEIVKRGK
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TVPSAOLFTTGYCEIPERDELSELQDLRLQRLMRISRETRDOOQAMLLSKTT
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ISAGKGVHLLDLELICALAGGQLEG"
2768. .3316
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Db 1450	ACTCGCGATCATCTTTCACATCGGCGCCGCACTCTCGCGGATATACCGTCTCCCT	1509		
QY 61	CCACCGGACCCCGCATGGTAGCGGCGACCTGCGGCTGCTGGGAAAGCTGATCATGCT	120		
Db 1510	CCACCGGACCCCGCATGGTAGCGGCGACCTGCGGCTGCTGGGAAAGCTGATCATGCT	1569		
QY 121	GATCGCGGCGCTCGGTCGCGGCGGCGGCGGCTCTCGGCTGCTCGGCGGCTCGGCTG	180		
Db 1570	GATCGCGGCGCTCGGTCGCGGCGGCGGCGGCTCTCGGCTGCTCGGCGGCTCGGCTG	1629		
QY 181	CGGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240		
Db 1630	CGGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1689		
QY 241	TGAGGTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCAC	300		
Db 1690	TGAGGTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCAC	1749		
QY 301	CGGTCGCAACTTGAAGCCCTTTTCGTCGCGGCTGTCACAGGTCGCGACAGTACGCA	360		
Db 1750	CGGTCGCAACTTGAAGCCCTTTTCGTCGCGGCTGTCACAGGTCGCGACAGTACGCA	1809		
QY 361	GTTGTTGACGCAAGTCACTGATTGGAAAGCGCATCGGCTGTGAGAAATGGTGTGCC	420		
Db 1810	GTTGTTGACGCAAGTCACTGATTGGAAAGCGCATCGGCTGTGAGAAATGGTGTGCC	1869		
QY 421	AGACCTATGGCTGGCACCAGCATCGGCGCTCGTTACCTTACTCTCTGTCCTTTAA	480		
Db 1870	AGACCTATGGCTGGCACCAGCATCGGCGCTCGTTACCTTACTCTCTGTCCTTTAA	1929		
QY 481	CTTAGCAAGGAC 492			
Db 1930	CTTAGCAAGGAC 1941			

BASE COUNT 669 a 1337 c 1060 g 695 t

ORIGIN

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Best Local Similarity 100.0%; Prid. No. 1.8e-73;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3556. >3761
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/db_xref="SPRMBL:004375"
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SSLEPYEKEFFVDSVRAVRDRLEDP"
SLEPYEKEFFVDSVRAVRDRLEDP"

RESULT 2

PSEANRPO 3761 bp DNA linear BCT 26-APR-1993

DEFINITION Pseudomonas aeruginosa anaerobic regulatory protein (aur) gene,
complete cds.

ACCESSION M98276

VERSION M98276.1 GI:151019

KEYWORDS aur gene; positive control element; regulatory protein.

SOURCE Pseudomonas aeruginosa (strain PAO1) DNA.

ORGANISM Pseudomonas aeruginosa

REFERENCE 1 (sites)

AUTHORS Zimmermann,A., Reilmann,C., Galimand,M. and Haas,D.

TITLE Anaerobic growth and cyanide synthesis of *Pseudomonas aeruginosa* depend on *anr*, a regulatory gene homologous with *fnr* of *Escherichia coli*

JOURNAL Mol. Microbiol. 5 (6), 1483-1490 (1991)

MEDLINE 92157874

PUBMED 1787798

REFERENCE 2 (sites)

AUTHORS Savioz, A., Zimmermann, A. and Haas, D.

JOURNAL RpoN-independent promoters having a conserved GG-N10-GC motif in *Pseudomonas aeruginosa*

REFERENCE Unpublished (1992)

AUTHORS 3 (bases 1 to 3761)

JOURNAL Zimmermann, A.

TITLE Anaerobe regulation des arginine-déaminase-opérons von *Pseudomonas aeruginosa* durch das protein *ANR*

JOURNAL Theses (1992)

FEATURES location/Qualifiers

source 1..3761

/organism="Pseudomonas aeruginosa"

/strain="PAO1"

/db_xref="taxon:287"

22..504

/note="ORF A; putative"

/number=1

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/translation="MLDTIRWDADLIRYDLSGPRYSPTAVAFHEGIGPEPDLAL RDSRKAHPISLYVHPFCANICYCACNVITTKDGRSPYLAIRLVREIETYSRHS RAQVYQHLHGSGGTPFLSPQDLRELSQLRHLNLDDSGYGLIDREADWSTK"

CDS 564..1061

/note="ORF B; putative"

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/db_xref="GI:151021"

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CDS complement(1235..1702)

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1948..2682

/gene="anr"

/function="anaerobic regulatory protein analog to *FNr* of *E. coli*"

/citation=[1]

/citation=[2]

/number=4

/codon_start=1

/evidence-experimental

/transl_table=11

/product="ANR"

/protein_id="AA25713.1"

/db_xref="GI:151023"

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CDS ISAEKKEVHLIDSTIELCALAGGLEC"

2768..3316

/note="analog to the apt gene of *E. coli*; ORF C; putative"

/number=5

/codon_start=1

/transl_table=11

/protein_id="AA25714.1"

/db_xref="GI:151024"

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3356..>3361

/note="ORF D; putative"

/number=6

/codon_start=1

/transl_table=11

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/db_xref="GI:151025"

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CDS

BASE COUNT 669 a 1337 c 1060 g 695 t

ORIGIN

Query Match 100.0%; Score 492; DB 1; Length 3761;

Best Local Similarity 100.0%; Pred. No. 1.8e-73;

Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTGCGGATCATCTTCACATCGCGCCCACTCTGCGGATATCCCTCGCTCCCT 60

DB 1450 ACTGCGGATCATCTTCACATCGCGCCCACTCTGCGGATATCCCTCGCTCCCT 1509

QY 61 CCACCGGACCCCATGGTAGCGGCAAGCTCGCCCTCGCTGGGAAAGCTGATCATGCT 120

DB 1510 CCACCGGACCCCATGGTAGCGGCAAGCTCGCCCTCGCTGGGAAAGCTGATCATGCT 1569

QY 121 GATCGCGGCGTGGTGGCGCGCGCGGCTTCCGCTGCTCGCGGCTGCGGCTCG 180

DB 1570 GATCGCGGCGTGGTGGCGCGCGCGGCTTCCGCTGCTCGCGGCTGCGGCTCG 1629

QY 181 CGGCGTGGCGTGGCGCGCGCGCGGCGGCAAGGCGGCACTGGGTGGTATCGACGAC 240

DB 1630 CGGCGTGGCGTGGCGCGCGCGCGGCGGCAAGGCGGCACTGGGTGGTATCGACGAC 1669

QY 241 TGAGGGTCAACATTCACATCGCGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 300

DB 1690 TGAGGGTCAACATTCACATCGCGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1749

QY 301 GCGTCGCACTTGAAGCCCTTTTCGTCGCCCTTGACAGGTCGACAGTATGCGCA 360

DB 1750 GCGTCGCACTTGAAGCCCTTTTCGTCGCCCTTGACAGGTCGACAGTATGCGCA 1809

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DB 1810 GTTGTGGAGCAAGTCACTGATGGAAAGGCAATCGGCGCTGAGAAATGCTGCTGCC 1869

QY 421 AGACCTATGCTGACACCGGATGCGGCTGCTTACCTTACCTTACCTTACCTTAA 480

DB 1870 AGACCTATGCTGACACCGGATGCGGCTGCTTACCTTACCTTACCTTAA 1929

QY 481 CCTAGCAAGGAC 492

DB 1930 CCTAGCAAGGAC 1941

RESULT 3

AE004582/c 11627 bp DNA linear BCT 30-AUG-2000

LOCUS Pseudomonas aeruginosa PAO1, section 143 of 529 of the complete genome.

ACCESSION AE004582 AE004091

VERSION AE004582.1 GI:9947492

KEYWORDS Pseudomonas aeruginosa.

SOURCE

ORGANISM Pseudomonas aeruginosa
Bacteria: Proteobacteria: gamma subdivision: Pseudomonadaceae;

REFERENCE 1 (bases 1 to 11627)
AUTHORS Stover,C.K., Pham,X.O., Erwin,A.L., Mizoguchi,S.D., Warrenner,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Xian,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Lardig,K., Lim,R., Smith,K., Spencer,D., Mong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
Nature 406 (6799), 959-964 (2000)

JOURNAL MEDLINE 20437337
PUBMED 10984043

TITLE 2 (bases 1 to 11627)
Stover,C.K., Pham,X.O., Erwin,A.L., Mizoguchi,S.D., Warrenner,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Xian,Y., Folger,K.R., Kas,A., Lardig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Mong,G.K., Wu,Z., Paulsen,I.T., Reizer,J., Sater,M.H., Hancock,R.E.W., Lory,S. and Olson,M.V.
Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA

FEATURES source 1. 11627
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QY 61 CCAACGGGACCCCGATGATGAGCGGCGAGCTGCGCCCTGCTGGGAAAGCTGATCATGCT 120
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QY 121 GATCGGGGGGCTGCTGCGCGCGCGCGGCTTCCGCTGCTGCGCGGTCGCGTCCGCTG 180
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QY 421 AGACCTATGGCTGCGACCCCGATGCGGCGCTTACCTTACCTCGTGTGCTTTAA 480
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Db 9468 AGACCTATGGCTGCGACCCCGATGCGGCGCTTACCTTACCTCGTGTGCTTTAA 9409
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Db 9408 CCTAGCAAGGAC 9397
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RESULT 4
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DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
protein_bind
gene
CDS
CDS
CDS

PAHEMN
P.aeruginosa hemm gene.
X97981
X97981.1
SI:1515307
ANR-binding motif; coproporphyrinogen III dehydrogenase; hemm gene;
ORFX.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
1 (bases 1 to 2635)
Hungerer,C., Troup,B., Raemling,U. and Jahn,D.
Cloning and regulation of the Pseudomonas aeruginosa hemm gene
encoding an oxygen-independent coproporphyrinogen III dehydrogenase
Unpublished
2 (bases 1 to 2635)
Jahn,D.
Direct Submission
Submitted (20-MAY-1996) D. Jahn, Laboratorium fuer Mikrobiologie,
Fachbereich Biologie, Philipps-Universitaet Marburg,
Karl-von-Frisch-Str., D-35032 Marburg, FRG
location/Qualifiers
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						Gaps	0

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Db 2415 CCACCGGACCCCATGGTGAAGGACGCTGGCCCTGCTGGGAAAGCTGACATGCT 2474

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 Db 2535 CGGCGTTGGCGTCGGCGGGCGCGGATGAGGGCGGCGACCTGGGTGGTGATCCAGCCAC 2594

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RESULT 5	PAANR	PAANR	LOCUS	900 bp	DNA	linear	BCR 14-ANT

DEFINITION *P. aeruginosa* ant gene for a transcriptional activator protein.

ACCESSION X58405

VERSION X58405.1 GI:45277

KEYWORDS ant gene; transcriptional activator

SOURCE
ORGANISM
Pseudomonas aeruginosa.
Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.

JOURNAL
TITLE
AUTHORS
REFERENCE
Submitted (11-MAR-1991) R. G. Sawers, Lehrstuhl f. Mikrobiologie
Direct Submission
Sawers, R.G.
1 (bases 1 to 900)

REFERENCE	2 (bases 1 to 900)
AUTHORS	Sawers, R.G.
TITLE	Identification and molecular characterization of a transcritic

JOURNAL
OF
MEDICAL
MICROBIOLOGY
5 (6), 1469-1481 (1991)

FEATURES	COMMENT	PUBLISHED
location/qualifiers	transcriptional activator of anaerobic gene expression which shows a high degree of amino acid similarity to FNR protein of <i>E. coli</i>	1/6/1971

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AC087547/c					
AC087547					
RESULT 6					

ACCESSION nbe004011, complete sequence.
AC087547
VERSION AC087547.2 GI:13184902
VERSION

SOURCE ORGANISM
Oryza sativa (Japonica cultivar-group) .
Oryza sativa (Japonica cultivar-group)
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliopsida: Dicotyledons: Rosales: Poaceae

REFERENCE
AUTHORS

Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 129420)
Llaca, V., Young, S., Kavchok, S., Charydczac, G., Ward, K. and
Mascetti, R.

TITLE
 Rice Chromosome 10
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 129420)
 AUTHORS
 Ilaya V. Koyanagi, Kenneth S. Church, et al.

TITLE
Nevill-Manning, C. and Messing, J.
Direct Submission
Submitted (08-JAN-2001) The Plant Genome Initiative at Rutgers -
Waksman Institute, Rutgers University, 100 Freilich Avenue, P.O. Box 231,
New Brunswick, NJ 08901-0231, USA
E-mail: jmessing@iml.rutgers.edu

REMARK	REFERENCE
Piscataway, NJ 08873	
Chromosome 10	
3 (bases 1 to 129420)	
154595 154596 154597 154598 154599 154600 154601 154602 154603 154604 154605 154606 154607 154608 154609 154610 154611 154612 154613 154614 154615 154616 154617 154618 154619 154620 154621 154622 154623 154624 154625 154626 154627 154628 154629 154630 154631 154632 154633 154634 154635 154636 154637 154638 154639 154640 154641 154642 154643 154644 154645 154646 154647 154648 154649 154650 154651 154652 154653 154654 154655 154656 154657 154658 154659 154660 154661 154662 154663 154664 154665 154666 154667 154668 154669 154670 154671 154672 154673 154674 154675 154676 154677 154678 154679 154680 154681 154682 154683 154684 154685 154686 154687 154688 154689 154690 154691 154692 154693 154694 154695 154696 154697 154698 154699 154700 154701 154702 154703 154704 154705 154706 154707 154708 154709 154710 154711 154712 154713 154714 154715 154716 154717 154718 154719 154720 154721 154722 154723 154724 154725 154726 154727 154728 154729 154730 154731 154732 154733 154734 154735 154736 154737 154738 154739 154740 154741 154742 154743 154744 154745 154746 154747 154748 154749 154750 154751 154752 154753 154754 154755 154756 154757 154758 154759 154760 154761 154762 154763 154764 154765 154766 154767 154768 154769 154770 154771 154772 154773 154774 154775 154776 154777 154778 154779 154780 154781 154782 154783 154784 154785 154786 154787 154788 154789 154790 154791 154792 154793 154794 154795 154796 154797 154798 154799 154800 154801 154802 154803 154804 154805 154806 154807 154808 154809 154810 154811 154812 154813 154814 154815 154816 154817 154818 154819 154820 154821 154822 154823 154824 154825 154826 154827 154828 154829 154830 154831 154832 154833 154834 154835 154836 154837 154838 154839 154840 154841 154842 154843 154844 154845 154846 154847 154848 154849 154850 154851 154852 154853 154854 154855 154856 154857 154858 154859 154860 154861 154862 154863 154864 154865 154866 154867 154868 154869 154870 154871 154872 154873 154874 154875 154876 154877 154878 154879 154880 154881 154882 154883 154884 154885 154886 154887 154888 154889 154890 154891 154892 154893 154894 154895 154896 154897 154898 154899 154900 154901 154902 154903 154904 154905 154906 154907 154908 154909 154910 154911 154912 154913 154914 154915 154916 154917 154918 154919 154920 154921 154922 154923 154924 154925 154926 154927 154928 154929 154930 154931 154932 154933 154934 154935 154936 154937 154938 154939 154940 154941 154942 154943 154944 154945 154946 154947 154948 154949 154950 154951 154952 154953 154954 154955 154956 154957 154958 154959 154960 154961 154962 154963 154964 154965 154966 154967 154968 154969 154970 154971 154972 154973 154974 154975 154976 154977 154978 154979 154980 154981 154982 154983 154984 154985 154986 154987 154988 154989 154990 154991 154992 154993 154994 154995 154996 154997 154998 154999 155000 155001 155002 155003 155004 155005 155006 155007 155008 155009 155010 155011 155012 155013 155014 155015 155016 155017 155018 155019 155020 155021 155022 155023 155024 155025 155026 155027 155028 155029 155030 155031 155032 155033 155034 155035 155036 155037 155038 155039 155040 155041 155042 155043 155044 155045 155046 155047 155048 155049 155050 155051 155052 155053 155054 155055 155056 155057 155058 155059 155060 155061 155062 155063 155064 155065 155066 155067 155068 155069 155070 155071 155072 155073 155074 155075 155076 155077 155078 155079 155080 155081 155082 155083 155084 155085 155086 155087 155088 155089 155090 155091 155092 155093 155094 155095 155096 155097 155098 155099 155100 155101 155102 155103 155104 155105 155106 155107 155108 155109 155110 155111 155112 155113 155114 155115 155116 155117 155118 155119 155120 155121 155122 155123 155124 155125 155126 155127 155128 155129 155130 155131 155132 155133 155134 155135 155136 155137 155138 155139 155140 155141 155142 155143 155144 155145 155146 155147 155148 155149 155150 155151 155152 155153 155154 155155 155156 155157 155158 155159 155160 155161 1	

TITLE
Messing, J.
Direct Submission
Submitted (02-MAR-2001) The Plant Genome Initiative at Rutgers -
Wakeland Institute Rutgers University, 100 Freeland Avenue, P.O.

REMARK	Piscataway, NJ 08873
COMMENT	Chromosome 10
REMARK	On Mar 2, 2001 this sequence version replaced g1:12044846.
REMARK	Location/Qualifiers

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1. 129420
/organism="Oryza sativa (japonica cultivar-group)"
/sub_species="japonica"
/db_xref="taxon:30047"
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Best Local Similarity	52.6%	Pred. No. 10;		
Matches 113; Conservative	0;	Mismatches 107;	Indels 0;	Gaps 0;

14 CTTCACCATGGCCGCAACTCTCTGGGGATATCTCTCTCTCTCTCTCACCGGCACCC 73

DB	Accession	Source	Organism	Reference Authors	Title	Journal	Remark
DB	90329	CGCGATCAATGCGCGGAGCGTCTTGAGACACCCCGCCGCGGACCGAGCAGCACCCTC	141041 bp	DNA	linear	PLN 30-MAY-2002	
QY	74	CATGATGACGGCCCACTGCGCCCTGCGTGGGAAGCTGTATCATGTCGGCGAGCTC	141041 bp	DNA	linear	PLN 30-MAY-2002	
DB	90269	CACGCGTCTGTCGCCACACAGCAGCAGGCTTCGCGCCCTCTCTCCGCGCGCGCGGAGG	141041 bp	DNA	linear	PLN 30-MAY-2002	
QY	134	GGTGGCGGCGCGCGGCTGCTGCGCTGCGCGCGGCTGCGCGCGCTGCGCGCGCTGCGCG	141041 bp	DNA	linear	PLN 30-MAY-2002	
DB	90209	CGGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141041 bp	DNA	linear	PLN 30-MAY-2002	
QY	194	CG	141041 bp	DNA	linear	PLN 30-MAY-2002	
DB	90149	CTCGGCG	141041 bp	DNA	linear	PLN 30-MAY-2002	
RESULT 7	AC087550	141041 bp	DNA	linear	PLN 30-MAY-2002		
LOCUS	AC087550/c						
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 10 clone						
ACCESSION	AC087550						
VERSION	AC087550.3						
KEYWORDS	HTG.						
SOURCE	Oryza sativa.						
ORGANISM	Oryza sativa.						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Erihartoideae; Oryzaceae; Oryza.						
AUTHORS	1 (bases 1 to 141041)						
TITLE	Oryza sativa (japonica cultivar-group) chromosome 10 clone						
JOURNAL	unpublished						
REFERENCE	2 (bases 1 to 141041)						
AUTHORS	Llaca, V., Young, S., Kavchok, S., Clark, T., Charydczac, G., Linton, E.,						
TITLE	Direct Submission						
JOURNAL	Submitted (08-JAN-2001) The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873						
REFERENCE	3 (bases 1 to 141041)						
AUTHORS	Llaca, V., Young, S., Kavchok, S., Ward, K., Charydczac, G. and Messing, J.						
TITLE	Direct Submission						
JOURNAL	Submitted (02-MAR-2001) The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873						
REFERENCE	4 (bases 1 to 141041)						
AUTHORS	Llaca, V., Song, R., Young, S., Kavchok, S., Ward, K. and Messing, J.						
TITLE	Direct Submission						
JOURNAL	Submitted (30-MAY-2002) The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873, USA						
COMMENT	On May 30, 2002 this sequence version replaced gi:13184872. This BAC overlaps with rice BAC nbcd004011 (AC087547) and nbcd0046p18 (AC087544).						
FEATURES	Location/Qualifiers						
SOURCE	1. 141041						
BASE COUNT	38213 a 31534 c 32795 g 38499 t						
ORIGIN							
Query Match	10.5%	Score 51.8	DB 8	Length 141041			
Best Local Similarity	52.6%	Pred. No. 9.8					
Matches 113	Conservative	0	Mismatches 102	Indels	0	Gaps	0

[illegible]

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RESULT 8
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LOCUS
DEFINITION
  Oryza sativa (japonica cultivar-group) chromosome 6 clone P0622F03.
ACCESSION
  ** SEQUENCING IN PROGRESS ***, in ordered pieces.
  AP003771
KEYWORDS
  AP003771.1 GI:14517645
SOURCE
  HTG, HTGS, PHASE2.
  Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
  clone:P0622F03.
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1
  Sasaki,T., Matsumoto,T. and Yamamoto,K.
  Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 6, PAC
  clone:P0622F03
  Published Only in Database (2001)
  2 (bases 1 to 175644)
  Sasaki,T., Matsumoto,T. and Yamamoto,K.
  Direct Submission
  Submitted (20-JUN-2001) Takuji Sasaki, National Institute of
  Agricultural Resources, Rice Genome Research Program, Kannondai
  2-1-2, Tsukuba, Ibaraki 305-8602, Japan
  (E-mail:tsasaki@agr.affrc.go.jp, URL:http://rjp.dna.affrc.go.jp/,
  Tel:81-298-38-7441, Fax:81-298-38-7468)
  NOTE: It currently consists of 1 contigs. Gaps between the contigs
  are represented as runs of N. The order of the pieces is believed
  to be correct as given, however the sizes of the gaps between them
  are based on estimates that have provided by the submitter. This
  sequence will be replaced by the finished sequence as soon as it is
  available and the accession number will be preserved.
  * NOTE: This is a 'working draft' sequence.
  * This sequence will be replaced
  * by the finished sequence as soon as it is available and
  * the accession number will be preserved.
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      /chromosome="6"
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BASE COUNT
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  Matches 105; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
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  db 85945 CCGCGGAAGCTCCGACACCGCCGCTCCCTTCACCGCGGCTGCTCGACAA 85886

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OY      62 CACCGGCAACCCCATGTAGACGGCCAGCTCGGCCCTGCCTGGAAAGTGTACATGGC 121
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DB 85885 GCGCGTGCCGTCCTTCCTCCGCCCCACCCTAGACTGCTCCGTCACAGCTGCTTTCCGTC 85826
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      122 ATCGGCGGCGTCGTCGCCGCGCGCGGCGGCTTCCTCCGTCGCGGCGTCGCCGTCGTC 181
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85825 ATCGCGCTGTCGTGTGTTTGTGTCGTCGTCCTCCCTCCCAAGGGGACCGGACAC 85766
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      182 GCGCTTGCGCGTCGCCGCG 198
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Db 85765 GCCGAGGAGGTCGCCGCG 85749
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RESULT 9
AC090435/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
Source

BASE COUNT
ORIGIN

Query Match
Best Local Similarity
Matches
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            57.4%: Pred. No. 28;
            0: Mismatches 66; Indels 0; Gaps 0;
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[illegible]


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Db      94215  CGGCGGCGCGCGCGCGCGCGCGCGGTCGACAGATGCGCGCGCGGTCGCGCGGCGTG  94274
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Db      94275  CTGCGTCGCGTCGTCGCGCGCGGTCGTACGCGCGCGCGCTGCGGCTGACAGTGCAGCGCGG  94334
Oy      169   TGCCGCTCGGTCGCGCGCGCTTGGCGTCGCGCGCGCGG  203
Db      94335  CGGCGGCGGCTGACGCGCGCGCGCGCGCGCGG  94369

RESULT 11
AF061246/c
LOCUS
DEFINITION
Ralstonia eutropha mutr and pntAA pseudogenes, complete sequence;
aspartate-1-decarboxylase (pand) gene, complete cds; and pntAB
pseudogene, complete sequence.
ACCESSION
AF061246
VERSION
AF061246.1
KEYWORDS
GI:3786393
SOURCE
Ralstonia eutropha.
Ralstonia eutropha
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
Ralstonia.
REFERENCE
1 (bases 1 to 3312)
Hoppensack,A., Rehm,B.H. and Steinbuechel,A.
Analysis of 4-phosphopantetheinylation of polyhydroxybutyrate
synthase from Ralstonia eutropha: generation of beta-alanine
auxotrophic Tm5 mutants and cloning of the pand gene region
J. Bacteriol. 181 (5), 1429-1435 (1999)
99175439
MEDLINE
10049372
PUBMED
2 (bases 1 to 3312)
Hoppensack,A., Steinbuechel,A. and Rehm,B.H.A.
Direct Submission
Submitted (23-APR-1998) Biology, Microbiology, Correnstr. 3,
Muenster, NRW 48149, Germany
FEATURES
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Best Local Similarity	56.0%	Pred. No. 48;							
Matches 93;	Conservative	0;	Mismatches 73;	Indels	0;	Gaps	0;		
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DB	1261	GATGACGACGGGGCGGGCTTCATCTGGCCAGTTCGGCGGCGCTGCGCGACCTT	1202						
OY	101	CTGGGAAGCTGTACATGCTGATCGCGCGCTGAGTCCGGCGCGGCGCTCCGCTG	160						
DB	1201	GAGCACACGACTGGGCGCCAGAGCTTCGGCGCGCTGCGCGAGTGTGGCGACCGACTC	1142						
OY	161	CTCGCGCGTCCGCGCTGCGCGCTTGGCGCTCCGCGCGCGCGCGC	206						
DB	1141	ATACCGCGCGTGGCTGGCTGACCGCGCGCGCGCGCTGC	1096						
RESULT 12									
AF033262/c									
LOCUS	AF033262	2450 bp	DNA	linear	BCT 05-OCT-2001				
DEFINITION	Pseudomonas sp. YD-15 endoglucanase gene, complete cds.								
ACCESSION	AF033262								
VERSION	AF033262.1	GI:4104165							
KEYWORDS									
SOURCE									
ORGANISM	Pseudomonas sp. YD-15.								
REFERENCE	Pseudomonas sp. YD-15.								
AUTHORS	Bacteria; Proteobacteria.								
	1 (bases 1 to 2450)								
	Her, S., Lee, H. S., Chol, S. J., Chol, S. W., Chol, H. J., Yoon, S. S. and Oh, D. H.								
TITLE	Cloning and sequencing of beta-1,4-endoglucanase gene (celA) from Pseudomonas sp. YD-15								
JOURNAL	Let. Appl. Microbiol. 29 (6), 389-395 (1999)								
MEDLINE	20128368								
PUBMED	10664983								
REFERENCE	2 (bases 1 to 2450)								
AUTHORS	Her, S., Lee, H. S. and Oh, D. H.								
TITLE	Direct Submission								
JOURNAL	Submitted (06-NOV-1997) Biotechnology, Yonsei University,								
SOEADAMUN-GU	Shincheon-Pong 134, Seoul 120-749, Korea								
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[Caenorhabditis elegans]; (residues 253..309); 67%
identity. predicted exon, program: grail2exons.human_1.3,
frame: 2, quality: excellent, score: 100.000-DDS
similarity to overlapping ESTs:
(1324..1168) T50998 yb71905.s1 Homo sapiens cDNA clone
76664.3' contains MER22 repetitive element; (280..124);
96% identity.-(1324..1167) W62177 m87d04.r1 Soares mouse
embryo NbME13.5 14.5 Mus musculus cDNA clone 375367.5'
similar to WP:116H12.5 CE00510 KRUPPEL-LIKE ZINC FINGER
PROTEIN ; (134..311); 87% identity.-(1324..1168) T51086
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2628..2926
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complement(3114..3414)
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complement(3428..3729)
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complement(3785..4102)
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4714..4747
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complement(5492..5611)
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[Caenorhabditis elegans]; (residues 209..252); 72%
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frame: 2, quality: excellent, score: 95.000-DDS similarity
to overlapping ESTs:
(5555..5492) T50998 yb71905.s1 Homo sapiens cDNA clone
76664.3' contains MER22 repetitive element; (344..281);
92% identity.-(5611..5492) W62177 m87d04.r1 Soares mouse
embryo NbME13.5 14.5 Mus musculus cDNA clone 375367.5'
similar to WP:116H12.5 CE00510 KRUPPEL-LIKE ZINC FINGER
PROTEIN ; (35..153); 84% identity.-(5555..5492) T51086
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repeat_region 8848..9143
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repeat_region 9150..9364
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repeat_region 11217..11333
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repeat_region 11636..11937
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Job time : 3143 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 06:59:43 ; Search time 2640 Seconds

(without alignments)
143.309 Million cell updates/sec

Title: US-09-548-449-8

Perfect score: 13

Sequence: 1 aatcaannantla 13

Scoring table:

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Total number of hits satisfying chosen parameters: 995600

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	10	76.9	24	6	AX226158
4	10	76.9	28	6	AX060375
5	10	76.9	28	6	AX085439
6	10	76.9	29	6	AR210200
7	10	76.9	29	6	AX402628
8	10	76.9	36	6	AR053365
9	10	76.9	36	6	AR053365
10	10	76.9	36	6	AR131089
11	10	76.9	36	6	AR131089
12	10	76.9	42	6	A04434
13	10	76.9	42	6	A05096
14	10	76.9	50	6	AX204152
15	10	76.9	50	6	AX204153
16	10	76.9	60	3	PEAPEP16DD
17	10	76.9	62	6	AX208903
18	10	76.9	65	6	AX482817
19	10	76.9	65	6	AX482818
20	10	76.9	65	6	AX482861
21	10	76.9	65	6	AX483043
22	10	76.9	65	6	AX483195
23	10	76.9	65	6	AX484722
24	10	76.9	65	6	AX484855
25	10	76.9	65	6	AX485630
26	10	76.9	77	8	QPE489833
27	10	76.9	87	6	AX241028
28	10	76.9	100	6	A43843
29	10	76.9	100	6	I17420
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31	9	69.2	17	6	A97808
32	9	69.2	17	6	AX263688
33	9	69.2	17	6	AX263689
34	9	69.2	17	6	AX428686
35	9	69.2	18	6	A97809
36	9	69.2	18	6	AR195307
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41	9	69.2	19	6	A97929
42	9	69.2	19	6	AX412034
43	9	69.2	19	6	AX428688
44	9	69.2	19	6	AX428807
45	9	69.2	20	6	AR089280

ALIGNMENTS

RESULT 1	AX132230	19 bp	DNA	linear	PAT 15-MAY-2001
LOCUS	AX132230				
DEFINITION	Sequence 3448 from Patent WO0130362.				
ACCESSION	AX132230				
VERSION	AX132230.1	GI:14138535			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 19)				
	Robbins, J.M. and Tritz, R.				
	Ribozyme therapy for the treatment of proliferative skin and eye diseases				

JOURNAL Patent: WO 0130362-A 3448 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES Location/Qualifiers
source 1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 7 AATCAAGACTTA 19

RESULT 2
A64535 24 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 27 from Patent W09726331.
DEFINITION A64535
ACCESSION A64535.1 GI:3717932
VERSION
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
FEATURES
REFERENCE 1 (bases 1 to 24)
AUTHORS Kornelik,R.G., Mackenzie,A.E., Roy,N., Robertson,G. and Tamal,K.
TITLE USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NIMP)
JOURNAL Patent: WO 9726331-A 27 24-JUL-1997;
UNIV OTTAWA (CA)
COMMENT Other publication AU 1614997 19970811.
FEATURES Location/Qualifiers
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/db_xref="taxon:32644"
ORIGIN

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Best Local Similarity 76.9%; Pred. No. 1.9e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTTA 13
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Db 8 AATCAATAAGTTA 20

RESULT 3
AX226158 24 bp DNA linear PAT 10-SEP-2001
LOCUS Sequence 77 from Patent W00160856.
DEFINITION AX226158
ACCESSION AX226158.1 GI:15555470
VERSION
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES
REFERENCE 1 (bases 1 to 24)
AUTHORS Vikkula,M.
TITLE vmgjom gene and its mutations causing disorders with a vascular
JOURNAL Patent: WO 0160856-A 77 23-AUG-2001;
UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 11 a 2 c 4 g 7 t

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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTTA 13
|||||
Db 9 AATCAAGACTTA 21

RESULT 4
AX060375 28 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 16 from Patent W00100819.
DEFINITION AX060375
ACCESSION AX060375.1 GI:12405861
VERSION
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES
REFERENCE 1 (bases 1 to 28)
AUTHORS Chauhan,S.
TITLE Targeted gene replacements in enteric bacteria using linear dna
JOURNAL Patent: WO 0100819-A 16 04-JAN-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US); GENENCOR INTERNATIONAL,
INC. (US)
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
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/note="primer"
ORIGIN

BASE COUNT 6 a 3 c 4 g 15 t

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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNNTTA 13
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Db 14 AATCAAGTAATTA 2

RESULT 5
AX085439 28 bp DNA linear PAT 09-MAR-2001
LOCUS Sequence 52 from Patent W00112833.
DEFINITION AX085439
ACCESSION AX085439.1 GI:13275494
VERSION
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES
REFERENCE 1 (bases 1 to 28)
AUTHORS Emplage,M., Hayne,S., Lafend,L., Puccl,J. and Whited,G.
TITLE Process for the biological production of 1,3-propanediol with high
JOURNAL Patent: WO 0112833-A 52 22-FEB-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US); GENENCOR INTERNATIONAL,
INC. (US)
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer-primer"
BASE COUNT 6 a 3 c 4 g 15 t

Query Match 76.9%; Score 10; DB 6; Length 28;
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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
Db 14 AATCAAGTAATTA 2

RESULT 6
LOCUS AR210200/c 29 bp DNA
DEFINITION Sequence 112 from patent US 6387652..
ACCESSION AR210200
VERSION AR210200.1 GI:21512370
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 112 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..29
BASE COUNT 7 a 0 c 7 g 15 t
ORIGIN

Query Match 76.9%; Score 10; DB 6; Length 29;
Best Local Similarity 76.9%; Pred. No. 1.8e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
Db 27 AATCAATCAATTA 15

RESULT 7
LOCUS AX402628/c 29 bp DNA
DEFINITION Sequence 112 from Patent W00196612.
ACCESSION AX402628
VERSION AX402628.1 GI:21387619
KEYWORDS
SOURCE Paecilomyces variotii.
ORGANISM Paecilomyces variotii.
REFERENCE 1
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 112 20-DEC-2001;
FEATURES Location/Qualifiers
source 1..29
BASE COUNT 7 a 0 c 7 g 15 t
ORIGIN

Query Match 76.9%; Score 10; DB 6; Length 29;
Best Local Similarity 76.9%; Pred. No. 1.8e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 27 AATCAATCAATTA 15

RESULT 8
LOCUS AR053365 36 bp DNA
DEFINITION Sequence 1 from patent US 5834236.
ACCESSION AR053365
VERSION AR053365.1 GI:5978227

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 36)
AUTHORS Lamb,C.J., Doerner,P. and Laible,G.
TITLE AATT repeat transcription enhancer element
JOURNAL Patent: US 5834236-A 1 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..36
BASE COUNT 16 a 1 c 2 g 17 t
ORIGIN

Query Match 76.9%; Score 10; DB 6; Length 36;
Best Local Similarity 76.9%; Pred. No. 1.7e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
Db 9 AATCAATTAATTA 21

RESULT 9
LOCUS AR053365/c 36 bp DNA
DEFINITION Sequence 1 from patent US 5834236.
ACCESSION AR053365
VERSION AR053365.1 GI:5978227
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 36)
AUTHORS Lamb,C.J., Doerner,P. and Laible,G.
TITLE AATT repeat transcription enhancer element
JOURNAL Patent: US 5834236-A 1 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..36
BASE COUNT 16 a 1 c 2 g 17 t
ORIGIN

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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 32 AATCAATTAATTA 20

RESULT 10
LOCUS AR131089 36 bp DNA
DEFINITION Sequence 1 from patent US 6191258.
ACCESSION AR131089
VERSION AR131089.1 GI:14119414
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 36)
AUTHORS Lamb,C.J., Doerner,P. and Laible,G.
TITLE Purified palindromic element binding factor
JOURNAL Patent: US 6191258-A 1 20-FEB-2001;
FEATURES Location/Qualifiers
source 1..36
BASE COUNT 16 a 1 c 2 g 17 t
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Db 9 AATCAATTATTA 21

RESULT 11
LOCUS ARI31089 36 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6191258.
ACCESSION ARI31089
VERSION ARI31089.1 GI:14119414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 36)
AUTHORS Lamb,C.J., Doerner,P. and Lalble,G.
TITLE Purified palindromic element binding factor
JOURNAL Patent: US 6191258-A 1 20-FEB-2001;
FEATURES Location/Qualifiers
source 1..36

BASE COUNT 16 a 1 c 2 g 17 t
ORIGIN

Query Match 76.9%; Score 10; DB 6; Length 36;
Best Local Similarity 76.9%; Pred. No. 1.7e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNNTTA 13
||||| |
Db 32 AATCAATTATTA 20

RESULT 12
LOCUS A04434 42 bp DNA linear PAT 29-APR-1993
DEFINITION Oligonucleotide U9 for salmon growth hormone.
ACCESSION A04434
VERSION A04434.1 GI:344937
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES Location/Qualifiers
source 1..42
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Best Local Similarity 76.9%; Pred. No. 1.7e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNNTTA 13
||||| |
Db 20 AATCAACAAGTTA 8

RESULT 13
LOCUS A05096 42 bp DNA linear PAT 30-APR-1993
DEFINITION Oligonucleotide L9 for salmon growth hormone.
ACCESSION A05096
VERSION A05096.1 GI:344983
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES Location/Qualifiers
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source 1..42
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Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNNTTA 13
||||| |
Db 4 AATCAACAAGTTA 16

RESULT 14
LOCUS AX204152 50 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 258 from Patent WO0148245.
ACCESSION AX204152
VERSION AX204152.1 GI:15393650
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Shinketsu,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0148245-A 258 05-JUL-2001;
Curegen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43967861"
variation 26
/note="single nucleotide polymorphism"

BASE COUNT 20 a 14 c 3 g 13 t
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Best Local Similarity 76.9%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNNTTA 13
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Db 24 AATCAACAAGTTA 36

RESULT 15
LOCUS AX204153 50 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 259 from Patent WO0148245.
ACCESSION AX204153
VERSION AX204153.1 GI:15393651
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Shinketsu,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0148245-A 259 05-JUL-2001;
Curegen Corporation (US)
FEATURES Location/Qualifiers
source 1..50


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/db_xref="taxon:9606"
misc_feature
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Accession number cg43967861"
variation
26
/note="single nucleotide polymorphism"
BASE COUNT
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Db 23 AATCAACAATTA 35

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Search completed: December 26, 2002, 13:25:58
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 08:20:51 ; Search time 54 Seconds
(without alignments)
97.797 Million cell updates/sec

Title: US-09-548-449-8
Perfect score: 13
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Gapop 10.0 , Gapext 1.0

Searched: 363474 segs, 203117208 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	10	76.9	44	10	US-09-839-743-28
6	10	76.9	62	10	US-09-777-564-743
7	10	76.9	65	10	US-09-783-590-1151
8	10	76.9	99	10	US-09-969-373-1158
9	9.6	73.8	78	10	US-09-764-877-445
10	9	69.2	20	8	US-08-983-605-453
11	9	69.2	20	10	US-09-758-881-20
12	9	69.2	20	10	US-09-452-599-39
13	9	69.2	22	9	US-09-835-371-46
14	9	69.2	22	10	US-09-860-784-25
15	9	69.2	24	9	US-10-014-436-10
16	9	69.2	24	10	US-09-969-373-3966
17	9	69.2	26	10	US-09-837-235-35
18	9	69.2	26	10	US-09-837-235-36
19	9	69.2	26	10	US-09-775-879-2

20	9	69.2	26	10	US-09-860-784-97	Sequence 97, Appl
21	9	69.2	26	10	US-09-860-784-98	Sequence 98, Appl
22	9	69.2	28	9	US-10-037-598-15	Sequence 15, Appl
23	9	69.2	33	10	US-09-955-462A-3	Sequence 3, Appl
24	9	69.2	40	9	US-09-832-292-25	Sequence 25, Appl
25	9	69.2	53	10	US-09-732-914-128	Sequence 128, Appl
26	9	69.2	64	10	US-09-865-807-50	Sequence 50, Appl
27	9	69.2	65	10	US-09-878-574-10483	Sequence 10483, A
28	9	69.2	67	8	US-08-808-031A-26	Sequence 26, Appl
29	9	69.2	68	10	US-09-983-965-154	Sequence 154, Appl
30	9	69.2	72	9	US-09-771-382-48	Sequence 48, Appl
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32	9	69.2	83	10	US-09-864-761-18906	Sequence 18906, A
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38	9	69.2	99	10	US-09-971-798-20	Sequence 20, Appl
39	9	69.2	99	10	US-09-971-798-21	Sequence 21, Appl
40	9	69.2	100	10	US-09-728-445-116	Sequence 116, Appl
41	8.4	64.6	15	10	US-09-504-231A-611	Sequence 611, Appl
42	8.4	64.6	15	10	US-09-274-553D-611	Sequence 611, Appl
43	8.4	64.6	20	9	US-09-774-223-4	Sequence 4, Appl
44	8.4	64.6	21	10	US-09-920-342-6	Sequence 6, Appl
45	8.4	64.6	22	8	US-08-913-322-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-913-322-27
Sequence 27, Application US/08913322
Patent No. US20020137028A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Roy, Natalie
APPLICANT: Robertson, George
APPLICANT: Tamaki, Katsu
TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
FILE REFERENCE: 07891/013001
CURRENT APPLICATION NUMBER: US/08/913, 322
CURRENT FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: PCT/IB97/00142
EARLIER FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: GB 9601108.5
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic primer based on Homo sapiens
US-08-913-322-27

Query Match 76.9%; Score 10; DB 8; Length 24;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTA 13
DB 8 AATCAATTAAGTTA 20

RESULT 2
US-09-839-743-1
Sequence 1, Application US/09839743
Patent No. US20020146824A1

```
GENERAL INFORMATION:
APPLICANT: The Salk Institute for Biological Sciences
APPLICANT: Lamb, Christopher
APPLICANT: Doerner, Peter
APPLICANT: Laidle, Goetz
TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
FILE REFERENCE: SALKINS.008DV3
CURRENT APPLICATION NUMBER: US/09/839,743
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/401,336
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 36
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-839-743-1
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```
Query Match          76.9%; Score 10; DB 10; Length 36;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 AATCAANNANTTA 13
    ||||| 1 |||
DB 9 AATCAATTATTA 21
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```
RESULT 3
US-09-839-743-1/c
Sequence 1, Application US/09839743
Patent No. US20020146824A1
GENERAL INFORMATION:
APPLICANT: The Salk Institute for Biological Sciences
APPLICANT: Lamb, Christopher
APPLICANT: Doerner, Peter
APPLICANT: Laidle, Goetz
TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and
TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
FILE REFERENCE: SALKINS.008DV3
CURRENT APPLICATION NUMBER: US/09/839,743
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/401,336
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 36
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-839-743-1
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Query Match          76.9%; Score 10; DB 10; Length 36;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 1 AATCAANNANTTA 13
    ||||| 1 |||
DB 32 AATCAATTATTA 20
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```
RESULT 4
US-09-839-743-28
Sequence 28, Application US/09839743
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```
Patent No. US20020146824A1
GENERAL INFORMATION:
APPLICANT: The Salk Institute for Biological Sciences
APPLICANT: Lamb, Christopher
APPLICANT: Doerner, Peter
APPLICANT: Laidle, Goetz
TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
FILE REFERENCE: SALKINS.008DV3
CURRENT APPLICATION NUMBER: US/09/839,743
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/401,336
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 44
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-839-743-28
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```
Query Match          76.9%; Score 10; DB 10; Length 44;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 AATCAANNANTTA 13
    ||||| 1 |||
DB 2 AATCAATTATTA 14
```

```
RESULT 5
US-09-839-743-28/c
Sequence 28, Application US/09839743
Patent No. US20020146824A1
GENERAL INFORMATION:
APPLICANT: The Salk Institute for Biological Sciences
APPLICANT: Lamb, Christopher
APPLICANT: Doerner, Peter
APPLICANT: Laidle, Goetz
TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and
TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
FILE REFERENCE: SALKINS.008DV3
CURRENT APPLICATION NUMBER: US/09/839,743
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/401,336
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 44
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-839-743-28
```

```
Query Match          76.9%; Score 10; DB 10; Length 44;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 AATCAANNANTTA 13
    ||||| 1 |||
DB 29 AATCAATTATTA 17
```

```
RESULT 6
US-09-777-564-743/c
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; Sequence 743, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannon, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 743
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-564-743

Query Match
Best Local Similarity 76.9%; Score 10; DB 10; Length 62;
Pred. No. 2.1e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
   ||||| | |||
Db 57 AATCAATAATTTA 45

RESULT 7
US-09-783-590-1151
; Sequence 1151, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.201
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1151
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-1151

Query Match
Best Local Similarity 76.9%; Score 10; DB 10; Length 65;
Pred. No. 2.1e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
   ||||| | |||
Db 11 AATCAATAATTTA 23

RESULT 8
US-09-969-373-1158/c
; Sequence 1158, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
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; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/855,768
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1158
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1158

Query Match
Best Local Similarity 76.9%; Score 10; DB 10; Length 99;
Pred. No. 2.1e+03;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
   ||||| | |||
Db 45 AATCAAGTAATTA 33

RESULT 9
US-09-764-877-445/c
; Sequence 445, Application US/09764877
; Patent No. US2002047140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 445
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-445

Query Match
Best Local Similarity 73.8%; Score 9.6; DB 10; Length 78;
Pred. No. 3.6e+03;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
   ||||| | |||
Db 47 AATCAAAAAAATTA 35

RESULT 10
US-08-983-605-453/c
; Sequence 453, Application US/08983605A
; Patent No. US2002006118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Trifolium aestivum and Tribe Trifolaceae and the Use of
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 20
; TYPE: DNA
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ORGANISM: Trifolium aestivum
US-08-983-605-453

Query Match 69.2%; Score 9; DB 8; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.5e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTT 12
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DB 15 AATCAATAAGTT 4

RESULT 11

US-09-758-881-20/c
Sequence 20, Application US/09758881
Patent No. US20010029250A1
GENERAL INFORMATION:
APPLICANT: Karitas, James G
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
FILE REFERENCE: ISPH-0532
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 09/288,461
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-20

Query Match 69.2%; Score 9; DB 10; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.5e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTT 12
|||||
DB 20 AATCAAGCAGTT 9

RESULT 12

US-09-452-599-39
Sequence 39, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Ouellette, Marc
TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-11
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-452-599-39

Query Match 69.2%; Score 9; DB 10; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.5e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AATCAANNANTTA 13
|||||
DB 5 AATCAACATTA 16

RESULT 13

US-09-835-371-46
Sequence 46, Application US/09835371
Publication No. US20020187473A1
GENERAL INFORMATION:
APPLICANT: UHLMANN, Eugen
APPLICANT: BREIPOHL, Gerhard
APPLICANT: WILL, David W
TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REFERENCE: 02481.1743 SEQUENCE LISTING
CURRENT FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: base sequence
US-09-835-371-46

Query Match 69.2%; Score 9; DB 9; Length 22;
Best Local Similarity 75.0%; Pred. No. 7.5e+03;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTT 12
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DB 2 AATCAATGACTT 13

RESULT 14

US-09-860-784-25
Sequence 25, Application US/09860784
Patent No. US20020151512A1
GENERAL INFORMATION:
APPLICANT: PEYMAN, Anuschirwan
UHLMANN, Eugen
TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,784
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,452
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 18748/264/HOCE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-860-784-25
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Query Match 69.2%; Score 9; DB 10; Length 22;
 Best Local Similarity 75.0%; Pred. No. 7.5e+03;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTT 12
 ||||| |
 Db 2 AATCAATGACTT 13

RESULT 15
 US-10-014-436-10
 ; Sequence 10, Application US/10014436
 ; Publication No. US20020182699A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HATADA, Yuji
 ; APPLICANT: IGARASHI, Kazuaki
 ; APPLICANT: OZAKI, Katsuya
 ; APPLICANT: AWA, Katsutoshi
 ; APPLICANT: KAWAI, Shuji
 ; APPLICANT: ITO, Susumu
 ; TITLE OF INVENTION: Gene for Enzyme Having Both Alkaline Pullulanase and Alkaline Amylase Activities
 ; FILE REFERENCE: 2173-0122P
 ; CURRENT APPLICATION NUMBER: US/10/014,436
 ; PRIOR FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: JP 111547/1995
 ; PRIOR FILING DATE: 1995-05-10
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01243
 ; PRIOR FILING DATE: 1996-05-10
 ; PRIOR APPLICATION NUMBER: US 08/952,084
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: US 09/514,302
 ; PRIOR FILING DATE: 2000-02-28
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer 4. Directed to Bacillus sp. used between XbaI to 1.2 kb u
 ; OTHER INFORMATION: psIream.
 US-10-014-436-10

Query Match 69.2%; Score 9; DB 9; Length 24;
 Best Local Similarity 75.0%; Pred. No. 7.6e+03;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTT 12
 ||||| |
 Db 12 AATCAAGAAATT 23

Search completed: December 26, 2002, 14:04:00
 Job time : 57 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 18:16:12 ; Search time 278 Seconds
(without alignments)
3985.551 Million cell updates/sec

Title: US-09-548-449-3
Perfect score: 492
Sequence: 1 actcgcgagatcatctcacc.....gccttaacctgaagac 492

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	492	100.0	492	21	AAZ58691 Pseudomonas ARN pr
3	492	100.0	492	22	ABA02573 Pseudomonas aerugi
4	47.8	9.7	1272	20	AA09010 Brn-3a polynucleot
5	47.8	9.7	1272	21	AAA29006 Human transcriptio
6	46.8	9.5	125401	22	AAD17186 Streptomyces nours
7	46	9.3	2765	22	AAHA1550 Human Rtl1 gamma n
8	46	9.3	3131	22	AAHA1549 Human Rtl1 beta nu
9	46	9.3	3332	22	AAHA1548 Human Rtl1 alpha'

C	10	46	9.3	3344	22	AAHA1505 Human Rtl1 encodin
C	11	45.6	9.3	530	21	AAA95215 Human OCT-11 parti
C	12	45.6	9.3	4524	20	AAV33912 Nucleotide sequenc
C	13	44.2	9.0	1146	16	AA083793 S. avermiltis BCK
C	14	44.2	9.0	2728	16	AA083797 S. avermiltis bkd
C	15	44	8.9	1388	23	ABV23346 human prostate exp
C	16	44	8.9	1388	23	ABV29200 human prostate exp
C	17	44	8.9	4257	19	AAV68520 The nucleotide seq
C	18	44	8.9	4257	19	AAV68520 The nucleotide seq
C	19	44	8.9	12001	16	AAO76213 HSV L/ST region.
C	20	43.8	8.9	68750	21	AAZ55887 Sorangium cellulos
C	21	43.8	8.9	71989	21	AAA29349 Sorangium cellulos
C	22	43.6	8.9	1424	23	ABL20183 Drosophila melanog
C	23	43.6	8.9	1469	23	ABL20181 Drosophila melanog
C	24	43.6	8.9	1502	23	ABL20117 Drosophila melanog
C	25	43.4	8.8	1131	22	AAH52039 Mycobacterium tube
C	26	43.4	8.8	1305	23	AAH54093 Pseudomonas aerugi
C	27	43.2	8.8	10468	23	ABL12316 Drosophila melanog
C	28	43.2	8.8	10468	23	ABL20180 Drosophila melanog
C	29	43.2	8.8	10468	23	ABL20182 Drosophila melanog
C	30	43.2	8.8	65140	22	AAAD17184 Streptomyces nours
C	31	42.8	8.7	367	20	AAZ19390 M. tuberculosis an
C	32	42.8	8.7	367	20	AAZ19178 M. tuberculosis re
C	33	42.8	8.7	1028	13	AAO27091 XTY26 probe. Homo
C	34	42.8	8.7	1028	22	AAH15342 Human Fragile X sy
C	35	42.8	8.7	1028	22	AAH15347 Human Fragile X sy
C	36	42.6	8.7	603	23	AAH78361 Chlamydomonas rein
C	37	42.4	8.6	2846	19	AAVA1260 Chlamydomonas rein
C	38	42.4	8.6	44377	18	AAAT78508 Platanolide synth
C	39	42.4	8.6	44377	18	AAAT80414 Platanolide synth
C	40	42	8.5	509	24	ABK34507 Human cDNA for nov
C	41	42	8.5	567	21	AAA29550 HIV codon altered
C	42	42	8.5	846	22	AAH06566 Human cDNA clone (
C	43	42	8.5	1651	24	AAH77281 Human hepatocyte g
C	44	42	8.5	2601	24	AAH28495 Human extracellular
C	45	42	8.5	3260	22	AAH17836 Human cDNA sequenc

ALIGNMENTS

RESULT 1	AAA95502 standard; DNA; 492 BP.
ID	AAA95502
AC	AAA95502;
DT	27-FEB-2001 (first entry)
DE	P. aeruginosa ANR promoter sequence.
DE	Bacteria: Infectio; drug-resistant pathogen; cancer; typhoid fever;
KW	bacterial meningitis; tuberculosis; antisense strand; ribozyme;
KW	toxic protein; ds.
OS	Pseudomonas aeruginosa.
PN	WO200061804-A1.
PD	19-OCT-2000.
PF	14-APR-2000; 2000WO-US10229.
PR	14-APR-1999; 99US-0291902.
PR	13-APR-2000; 2000US-0548445.
PA	(MUSC-) MUSC FOUND RES DEV.
PA	(UNPE-) UNIV PENN STATE.
PI	Norris J, Clawson G, Westwater C, Schofield D, Schmidt M, Hoel B;
PI	Dolan J, Pan W;
DR	WPI: 2000-638570/61.

Db 241 TGAAGTCACATTCACAGTCCGCGGAAAAATGAAATTCCTTCATTGATCGGCCAC 300
 QY 301 GCGTCGGCAACTTACAGCCCTTTCTGTCGCCCTTGACAGGTGCGACAGTAGTCGCA 360
 Db 301 GCGTCGGCAACTTACAGCCCTTTCTGTCGCCCTTGACAGGTGCGACAGTAGTCGCA 360
 QY 361 GTTGTTCAGCAAGTACATTCATTTGAAAGCCATTCGGCTGTAGAAATGTGTGCC 420
 Db 361 GTTGTTCAGCAAGTACATTCATTTGAAAGCCATTCGGCTGTAGAAATGTGTGCC 420
 QY 421 AGACCTATGCTGGCACCACCCGATCGGCTGCGTTACCTTACTCTGTTGTGCTTTAA 480
 Db 421 AGACCTATGCTGGCACCACCCGATCGGCTGCGTTACCTTACTCTGTTGTGCTTTAA 480
 QY 481 CCTAGCAAGGAC 492
 Db 481 CCTAGCAAGGAC 492

RESULT 3
 ABA02573 standard; DNA; 492 BP.
 ABA02573:
 XX ABA02573:
 AC ABA02573:
 DT 05-FEB-2002 (first entry)
 XX
 XX Pseudomonas aeruginosa promoter ANR.
 DE
 XX Infection; antisense RNA; ribozyme; DNAzyme; antiviral; gene therapy;
 KM papilloma virus; hepatitis B virus; cytotoxic; cytostatic; warty;
 KM cervical dysplasia; cervical carcinoma; carcinoma; laryngeal papilloma;
 KM ANR promoter; ds.
 XX
 XX Pseudomonas aeruginosa.
 OS
 XX
 XX WO200179524-A2.
 PD 25-OCT-2001.
 XX
 XX 13-APR-2001; 2001WO-US12130.
 PF
 XX
 XX 13-APR-2000; 2000US-0548449.
 PR 07-DEC-2000; 2000US-251810P.
 XX
 XX (UYSC-) UNIV SOUTH CAROLINA.
 PA (PENN-) PENN STATE RES FOUNO.
 XX
 PI Norris JS, Clawson GA, Westwater C, Schofield D, Schmidt WG;
 PI Hoel B, Dolan J, Pan W;
 DR WPI; 2001-607700/69.
 XX
 XX Novel nucleic acid for the treatment of papilloma or hepatitis virus
 PT induced conditions comprises a catalytic region which produces a
 PT cytotoxic or cytostatic effect in the infected cell -
 XX
 XX Examples; Fig 1; 143bp; English.

The invention relates to the discovery, identification and
 CC characterization of toxic agents lethal to pathogens and methods for
 CC targeting such toxic agents to a pathogen or pathogen infected cells in
 CC order to treat and/or eradicate the infection. In particular the
 CC invention relates to at least one nucleic acid molecule, which
 CC specifically hybridises to mRNA encoding at least one viral protein
 CC associated with the transformation of plasmid copy number control, which
 CC hybridises to a viral polyadenylation signal or a core, pre core or
 CC polymerase encoding sequence. Specifically, the invention relates to the
 CC delivery of one or more toxic gene products, antisense RNAs, ribozymes,
 CC DNAzymes or a combination thereof. The nucleic acids have antiviral
 CC activity and can be used in gene therapy. They are useful for the
 CC treatment of papilloma or hepatitis virus induced conditions and can
 CC produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis B

CC infected cells. The papilloma virus induced condition is selected from
 CC warts, cervical dysplasia, cervical carcinoma, carcinoma in situ and
 CC laryngeal papilloma. The present sequence is that of a Pseudomonas
 CC aeruginosa promoter sequence, useful to the invention.
 XX

Sequence 492 BP: 77 A; 164 C; 147 G; 104 T; 0 other:
 SQ

Query Match 100.0%; Score 492; DB 22; Length 492;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTGCGGATCATCTTACCATTCGCGCAATCTCTCGGGATTCCTGCTCTCTCT 60
 Db 1 ACTGCGGATCATCTTACCATTCGCGCAATCTCTCGGGATTCCTGCTCTCTCT 60
 QY 61 CCACCGGACCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 61 CCACCGGACCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 121 GATCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 121 GATCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 CGGCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 CGGCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 TGAGGTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACAT 300
 Db 241 TGAGGTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACAT 300
 QY 301 GCGTCGGCAACTTACAGCCCTTTCTGTCGCCCTTGACAGGTGCGACAGTAGTCGCA 360
 Db 301 GCGTCGGCAACTTACAGCCCTTTCTGTCGCCCTTGACAGGTGCGACAGTAGTCGCA 360
 QY 361 GTTGTTCAGCAAGTACATTCATTTGAAAGCCATTCGGCTGTAGAAATGTGTGCC 420
 Db 361 GTTGTTCAGCAAGTACATTCATTTGAAAGCCATTCGGCTGTAGAAATGTGTGCC 420
 QY 421 AGACCTATGCTGGCACCACCCGATCGGCTGCGTTACCTTACTCTGTTGTGCTTTAA 480
 Db 421 AGACCTATGCTGGCACCACCCGATCGGCTGCGTTACCTTACTCTGTTGTGCTTTAA 480
 QY 481 CCTAGCAAGGAC 492
 Db 481 CCTAGCAAGGAC 492

RESULT 4
 AAX09010 standard; cDNA; 1272 BP.
 ID AAX09010
 XX
 AC AAX09010:
 XX
 DT 14-JUN-1999 (first entry)
 XX
 XX Brn-3a polynucleotide.
 DE
 XX Brn-3a; Bcl-2; neurone; neuronal cells; apoptosis; cell death; CNS;
 KW PNS; central nervous system; parasympathetic nervous system;
 KW development; injury; neurotrophic factor; nerve growth factor; NGF;
 KW ciliary neurotrophic factor; CNTF; brain-derived neurotrophic factor;
 KW BDNF; neurotrophin; NT-3; NT-4; NT-5; neurodegenerative disease;
 KW familial dysautonomia; infantile muscular dystrophy;
 KW Parkinson's disease; Alzheimer's disease; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key location/Qualifiers
 FH CDS 1..1272
 FT /*tag= a
 FT /product= Brn-3a-polypeptide
 XX

PN M09905272-A1.
XX
PD 04-FEB-1999.
XX
PF 27-JUL-1998; 98WO-GB02228.
XX
PR 10-DEC-1997; 97US-0988476.
XX 25-JUL-1997; 97GB-0015823.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Latchman DS, Smith MD;
XX
DR WPI: 1999-142928/12.
XX P-PSDB; AAM96262.
XX
PT New polypeptide comprising transcription factor Brn-3a, or its
PR derivative - useful for treating nervous system diseases, preventing
PP cellular apoptosis and increasing nerve regeneration following
PT neuronal damage

Disclosure: Page 61-62; 68pp; English.

Over expression of transcription factor Brn-3a can protect neuronal cells from apoptosis. Brn-3a also specifically activates expression of the Bcl-2 gene in neuronal cells and this activation is mediated via a Brn-3a response element in the 5' regulatory region of the Bcl-2 gene. Both the anti-apoptotic effect of Brn-3a and its ability to activate expression of Bcl-2 are mediated by the N-terminal domain of Brn-3a. Members of the Bcl-2 family perform critical roles in the regulation of selective apoptosis during development of the nervous system. The stimulation of Bcl-2 expression by Brn-3a in a neuron specific manner and consequent protection of neuronal cells from apoptosis suggests that Brn-3a may co-ordinate some aspects of neuronal reorganisation during development or following injury. The elevation of Brn3a expression by either pharmacological means (compositions comprising one other therapeutic polypeptide e.g. neurotrophic factors, nerve growth factor (NGF), ciliary neurotrophic factor (CNTF), brain-derived neurotrophic factor (BDNF), and neurotrophins NT3 and NT-4/5) or gene therapy may represent a method for treating human diseases associated with excessive neuronal cell death and/or lack of nerve regeneration, especially neurodegenerative diseases such as familial dysautonomia and infantile muscular dystrophy, and Parkinson's and Alzheimer's disease.

Sequence 1272 BP: 202 A; 468 C; 452 G; 150 T; 0 other;

Query Match 9.7%; Score 47.8; DB 20; Length 1272;
Best Local Similarity 50.2%; Pred. No. 0.081

Matches 118; Conservative 0; Mismatches 117; Indels 0; Gaps 0

2 CTCGGGATCATCTTCACCATGAGCGGCACAACCTCGGGATATCCTCTCCCTCTC 61
|| || || || || || || || || || || || || || || || || || || ||
Db 292 CTGGCGCACACACCACACACACCAACCAACCAACCAAGGCCGTGAAACCGCGCATCTGCG 351

QY 62 CACCGGACACCCCATATGTAAGAGCGGCAAGCTGCGGCCCTGCTTGGGAAGCTGATATGCTG 121
|| || || || || || || || || || || || || || || || || || || ||
Db 352 GACCAACATCTCTCCCTCCCTGCTGCTGCTCAATGAGCGGCGGCGCGCGCGCGCGG 411

QY 122 ATCGCGCGGCTGAGTGCGCGGCGGCGGCTTCCTCGCATCTCGGCGCGTCCGGTCCGTG 181
|| || || || || || || || || || || || || || || || || || || ||
Db 412 GGCGGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 471

QY 182 GGCCTTGGCGTCCGCGGCGGCGCGATGAGGCGGCGACCATCTGGGTGTGATCCAG 236
|| || || || || || || || || || || || || || || || || || || ||
Db 472 GGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526

RESULT 5
AAA29006
ID AAA29006 standard; CDNA; 1272 BP.
XX

[illegible]

RESULT	6
AAD17186/c	
ID	AAD17186 standard; DNA; 125401 BP.
XX	
AC	AAD17186;
XX	
DT	29-NOV-2001 (first entry)
XX	
DE	Streptomyces noursei nystatin PKS gene cluster DNA.
XX	
KW	Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
KW	antifungal; antibiotic; ds.
XX	
OS	Streptomyces noursei.
XX	
FH	Key
FH	Location/Qualifiers
FH	CDS
FT	/tag- a
FT	/product- "NysI complete protein"
FT	34792..51099
FT	/tag- b
FT	/product- "NysJ protein"
FT	51155..57355
FT	/tag- c
FT	/product- "NysK protein"
FT	57503..58687
FT	/tag- d
FT	/product- "NysL protein"
FT	complement (58786..58980)
FT	/tag- e
FT	/product- "NysM protein"
FT	/note- "CDS does not include start codon"
FT	/tag- f
FT	/product- "NysN protein"
FT	/note- "CDS does not include start codon"
FT	complement (60238..61296)
FT	/tag- g
FT	/product- "NysD2 complete protein"
FT	120628..121308
FT	/tag- h
FT	/product- "NysR4 (long) protein"
XX	
PN	MO200159126-A2.
XX	
PD	16-AUG-2001.
XX	
PF	08-FEB-2001; 2001WO-GH0509.
XX	
PR	08-FEB-2000; 2000GB-0002840.
PR	10-APR-2000; 2000GB-0008786.
PR	14-APR-2000; 2000GB-0009387.
XX	
PA	(UNIV-) UNIV NORGES TEKNISK NATURVITTENSKAPELIGE.
PA	(SWEF-) SINTER STIPTELSEN IND TEK FORSK.
PA	(ALPH-) ALPHARMA AS.
PA	(SINV-) SINVENT AS.
PA	(IDIE/) DZIEGLEWSKA H.
PA	(ZOTC/) ZOTCHEV S B.
PA	(SEKU/) SEKUROVA O N.
PA	(FJAE/) FJAERVIK E.
PA	(BRAU/) BRAUTASET T.
PA	(STRO/) STROM A R.
XX	
PI	Zotchev SB, Sekurova ON, Fjaervik E, Brautaset T, Strom AR;
PI	Valla S, Ellingsen TE, Sletta H, Gulliksen O;
DR	WP1: 2001-557614/62.
DR	P-PSDB: AAEE10143, AAEE10144, AAEE10145, AAEE10146, AAEE10147, AAEE10148,
XX	AAE10149, AAE10150.
XX	
PT	New nystatin polyketide synthase polynucleotides and polypeptides,

```

PR useful as antibiotics and antifungals -
XX
PS Claim 1; Page 188-254; 266pp; English.
XX
CC The present invention relates to the cloning and sequencing of the gene
CC cluster encoding a modular type I polyketide synthase (PKS) enzyme
CC involved in the biosynthesis of the macrolide antibiotic nystatin.
CC The nystatin PKS is useful as antifungal antibiotics. The present
CC sequence is a Streptomyces noursei nystatin PKS gene cluster DNA.
XX
SQ Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;

Query Match 9.5%; Score 46.8; DB 22; Length 125401;
Best Local Similarity 52.6%; Pred. No. 0.26;
Matches 102; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

OY 23 GCGCGCGCAACTCTCGGGATATCCTTCGTCCTCCTCCTCACCAGCCCATGATGTAAC 82
DB 44196 CCGTACCGCGGTGTCGCGCCGTGCTCTCGTGAAGCCGAGACAGGAGACACGCGGTGCG 44137
OY 83 GGCACGACTGCGCCCTGCTGGGAAAGCTGTACATGCTGATCGCGCGGTGCGGTGCGGC 142
DB 44136 GCGCGGTGTCGTGGCGCCGCTTCGTGAGCAAGGCGGCGAGCGCGGCCGCTCGTCCGTG 44077
OY 143 GCGCGCGGTCTTCGCGCTGCTCGCGGATGCGCGGTGCGCGGCTTGACGTCGCCGCGCGC 202
DB 44076 GCGCGGAGACGTCCACCGCGGCGGTGCGGCGGAGGCGGCGAGAGAGCTGCGGCACCA 44017
OY 203 GCGCATGAGGCGG 216
DB 44016 GGGGTGCGGTGTCG 44003

RESULT 7
AAH41550/c
ID AAH41550 standard; DNA; 2765 BP.
XX
AC AAH41550;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human Rlt1 gamma nucleotide sequence.
XX
KW Mouse; human; combined DNA/RNA molecule; Rlt1; tumour suppressor;
KW 2-3 type zinc finger structure; cancer; diagnosis; carcinogenesis;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 11..2116
FH FT /*tag=a
FT /product="Rlt1 gamma"
XX
PN WO200132859-A1.
XX
PD 10-MAY-2001.
XX
PF 14-JUL-2000; 2000WO-JP04765.
XX
PR 29-OCT-1999; 99JP-0310420.
XX
PA (MOCH ) MOCHIDA PHARM CO LTD.
XX
PI Komlunani R;
XX
DR WPI: 2001-316438/33.
XX
DR P-PSDB: AAB99341.
XX
PT New zinc finger protein and gene encoding it for detecting and
PT diagnosing cancer, estimating the risk of carcinogenesis, and for gene
PT therapy -
XX

```


PT	therapy
XX	
PS	Claim 38; Page 73-76; 119pp; Japanese.
CC	
XX	The present invention describes a combined DNA/RNA molecule designated
CC	Rit1, which has a 2-3 type zinc finger structure and tumour suppressor
CC	activity. Rit1 has cytostatic activity and can be used in gene therapy.
CC	Genomic or cDNA encoding Rit1 can be used in the detection and diagnosis
CC	of cancer, and the estimation of the risk of carcinogenesis. Rit1 and
CC	its partial peptides are also used to detect and diagnose cancer, and
CC	estimate the risk of carcinogenesis. The present sequence encodes
CC	human Rit1 alpha', from the present invention.
XX	
SQ	Sequence 3332 BP; 637 A; 1113 C; 1036 G; 534 T; 12 other;
Query Match	9.3%; Score 46; DB 22; Length 3332;
Best Local Similarity	50.5%; Pred. No. 0.25;
Matches 112; Conservative	0; Mismatches 110; Indels 0; Gaps 0;
OY	32 CTCCTGCGGGATATTCCTGCTCCTCTCTCCACCGCGCACCCCCAGTGAAGGCCACTGC 91
Db	1639 CTTCGTAGACAGCT 1580
OY	92 GCGCCCTGCGGGAAAGCTGTACATGCTGATCGGCGGCGTGCGGCGCGCGCGCGCGTC 151
Db	1579 GCCCAGCAGCGGGTCCCTCTCTGTTGGGGAGAATCACCCTGCGCCCTTAGGCCCTTC 1520
OY	152 TTCCGCTGCTGCGCGGTCGCGGTCCTGTCGCGGCTTGGCGTCGCGGCGCGCGCATGA 211
Db	1519 GCCCGCAGCTCGCTGCTGCTGCGCGGCGCGGAGCTGCGGCGCGAGAGCCCTCTCGTCA 1460
OY	212 GGGCGGCACCTGGTGGTGTGATCAGCCACTGAGGTCACAAT 253
Db	1459 GCGCGCGCGCAGCGAGCGCGCTTGTGATGTGCGTCTTCA 1418
RESULT 10	
AAH41505/c	
ID	AAH41505 standard; DNA: 3344 BP.
XX	
AC	AAH41505;
XX	
DT	14-SEP-2001 (first entry)
XX	
DE	Human Rit1 encoding DNA SEQ ID NO:3.
XX	
KW	Mouse; human; combined DNA/RNA molecule; Rit1; tumour suppressor;
KW	2-3 type zinc finger structure; cancer; diagnosis; carcinogenesis;
KW	gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 11..2695
FT	/*tag= a
FT	/product= "Rit1"
XX	
PN	WO200132859-A1.
XX	
PD	10-MAY-2001.
XX	
PF	14-JUL-2000; 2000WO-JP04765.
XX	
PR	29-OCT-1999; 99JP-0310420.
XX	
PA	(MOCH) MOCHIDA PHARM CO LTD.
XX	
PI	Kominami R;
XX	
DR	WPI; 2001-316438/33.
XX	
DR	P-PADB; AAB99335.
XX	
PT	New zinc finger protein and gene encoding it for detecting and

PT	diagnosing cancer, estimating the risk of carcinogenesis, and for gene therapy
PS	Claim 8; Page 103-108; 119pp; Japanese.
XX	
XX	The present invention describes a combined DNA/RNA molecule designated Rtl1, which has a 2-3 type zinc finger structure and tumour suppressor activity. Rtl1 has cytosstatic activity and can be used in gene therapy.
CC	Genomic or cDNA encoding Rtl1 can be used in the detection and diagnosis of cancer, and the estimation of the risk of carcinogenesis. Rtl1 and its partial peptides are also used to detect and diagnose cancer, and estimate the risk of carcinogenesis. The present sequence encodes human Rtl1.
CC	
XX	
XX	Sequence 3344 BP; 639 A; 1115 C; 1040 G; 538 T; 12 other;
XX	
Query Match	9.3%; Score 46; DB 22; Length 3344;
Best Local Similarity	50.5%; Pred. No. 0.25;
Matches 112; Conservative	0; Mismatches 110; Indels 0; Gaps 0;
QY	32 CTCGCGGGATATCCTGCTCCTCCTCCACCGGACCCCATGTAGCGCCAGCTC 91
Db	1651 CTCGAGTAGAGACCTCTCCTCCTCCTCCGTCGTCGTCCTCCTCCTCGGCTCGTG 1592
QY	92 GCGCCCTCCTGGGAAAGCTGTACATGCTGATGGCGGCGCTGCTGCGCGCCGCTC 151
Db	1591 GCCCGACGACGGGTGCTCTCTGTGGGGAAAGTACACGTCGGCCGCTTGAGGCCCTC 1532
QY	152 TTCGCGCTGCTGGGGGTCGCGGCTGTCGCGGCTTGCGGCTGGCGGCGCGCGATGA 211
Db	1531 GCCCGCAGCTGCTGCTGCTGCTGCGGCTCGGGGAGCTGGCGGCGCGAGCCCTGCTGGA 1472
QY	212 GGGCGGACCTGGGTGTGATCCAGCCACTGAGGGTCAACAT 253
Db	1471 GCGCGCGGCGCAGCGAGCGGCTGTGCATGTGCGTCTTCA 1430
RESULT 11	
ID	AAA95215
AC	AAA95215 standard; cDNA; 530 BP.
XX	
AC	AAA95215;
DT	12-JAN-2001 (first entry)
XX	
DE	Human OCT-T1 partial coding sequence.
XX	
OS	Homo sapiens.
XX	
PN	US6114150-A.
XX	
PD	05-SEP-2000.
XX	
PF	02-DEC-1996; 96US-0758662.
XX	
PR	29-NOV-1995; 95US-0564653.
PA	(UYYA) UNIV YALE.
XX	
PI	Weissman SM, Baskaran N;
XX	
DR	WPI; 2000-586478/55.
XX	
PT	Uniform amplification of heterogeneous mixture of nucleic acid templates of varying G+C content, comprises amplifying the reaction mixture in the presence of betaine and dimethyl sulphoxide
XX	
XX	Example 1; column 13-14; 15pp; English.

XX The present sequence is the coding sequence for the human T lymphocyte
 CC octamer binding protein OCT-1. It was used as a test sequence in an
 CC assay to demonstrate the method of the invention, which involves a novel
 CC way of amplifying GC rich nucleic acids. In addition to the normal
 CC mixture a zwitterion and a compound which disrupts base pairing are added
 CC to the PCR reaction. The zwitterion is preferably betaine (trimethyl
 CC glycine), D-carnitine, dimethyl glycine or monomethyl glycine, and the
 CC base pair disruption compound may be DMSO, formamide, sodium perchlorate
 CC or glyoxyl, among others. This method is useful as it allows the uniform
 CC and more efficient amplification of nucleic acids composed of GC rich
 CC regions. This is useful in DNA library construction, as the 5' end of
 CC genes are often GC rich, and in the diagnosis of diseases where GC rich
 CC triplets are expanded, for example fragile X syndrome, spinobular
 CC muscular atrophy, myotonic dystrophy, Huntington's disease and
 CC spinocerebellar ataxia type 1.

SO Sequence 530 BP; 61 A; 215 C; 203 G; 51 T; 0 other;

Query Match 9.3%; Score 45.6; DB 21; Length 530;

Best Local Similarity 54.3%; Pred. No. 0.24;

Matches 113; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

QY 22 TCGGCGGCAACTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 81
 DB 264 TGGACACATCTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 323
 QY 82 CGGCGAGCTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 140
 DB 324 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 383
 QY 141 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 200
 DB 384 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 443
 QY 201 GCGGCGGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 228
 DB 444 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 471

RESULT 12

ID AAV33912 standard; cDNA; 4524 BP.

XX AAV33912;

DT 12-FEB-1999 (first entry)

DE Nucleotide sequence of the SIAX DP2-64 (Oct-T1) gene.

KM Tumour rejection antigen precursor; TRAP; TRH; leukaemia; screening;
 KM lymphoma; cancer; HLA; human lymphocyte antigen; vaccine;
 KM SIAX DP2-64; Oct-T1; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 174..1436

FT /*tag= a

PN WO9849299-A1.

PD 05-NOV-1998.

PF 22-APR-1998; 98WO-US07784.

PR 25-APR-1997; 97US-0845998.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon-Falleur T, Coulie PG, De Smet C, Lucas S, Van Baren N;

PI WPI: 1999-009425/01.

DR P-PsDB: AAM68541.
 XX New diagnosis of leukaemia - by detecting genes for tumour antigen
 PT rejection precursors or corresponding proteins
 PS Claim 1; Pages 63-67; 88pp; English.

XX The present sequence represents the nucleotide sequence of the
 CC SIAX DP2-64 (Oct-T1) gene. The protein is a tumour rejection
 CC antigen precursor (TRAP). The specification describes the treatment of
 CC disorders which characterised by expression of a leukaemia-associated
 CC nucleic acid such as TRH. The products are used for in vivo or in vitro
 CC screening for leukaemia, lymphoma or other cancers by usual
 CC hybridisation/amplification or immunoassay methods. TRAPs, when
 CC processed to antigens or complexed with HLA (human lymphocyte antigen)
 CC molecules, or nucleic acid encoding them, are useful in vaccines for
 CC treating leukaemia.

SO Sequence 4524 BP; 1177 A; 1090 C; 1180 G; 1077 T; 0 other;

Query Match 9.3%; Score 45.6; DB 20; Length 4524;

Best Local Similarity 54.3%; Pred. No. 0.32;

Matches 113; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

QY 22 TCGGCGGCAACTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 81
 DB 523 TGGACACATCTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 582
 QY 82 CGGCGAGCTCTGCGGATATCTCTGCTCCCTCCACCGGACCCCATGCTAG 140
 DB 583 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 642
 QY 141 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 200
 DB 643 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 702
 QY 201 GCGGCGGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 228
 DB 703 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 730

RESULT 13

ID AA083793/C standard; cDNA; 1146 BP.

XX AA083793;

DT 05-SEP-1995 (first entry)

DE S. avermitilis BCKDH El-alpha subunit.

KM Branched-chain alpha-keto-acid-dehydrogenase; BCKDH; bkd gene;
 KM avermectin; antibiotic; acaricide; anthelmintic; insecticide;
 KM nematocide; pesticide; ds.

OS Streptomyces avermitilis.

FT Key Location/Qualifiers

FT CDS 1..1146

FT /*tag= a

PN WO9504150-A.

PD 09-FEB-1995.

PF 30-MAY-1994; 94WO-IB00127.

PR 30-JUL-1993; 93US-0100518.

XX (Pfizer) PFIZER INC.

PI Denoya CD;


```
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4234-4235; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 1388 BP; 205 A; 445 C; 377 G; 338 T; 23 other:

Query Match      8.9%; Score 44; DB 23; Length 1388;
Best Local Similarity 52.7%; Pred. No. 0.63;
Matches 118; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY      8 GATCATCTTCACCATCGCGCCGCAACTCTGCGGATATCCTGCTCCTCCTCACGG 67
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1148 GTTCTCTTCGCGGATGCGCTGCTTCATCTGCTCCATCTGCTGCGCTGCTCCGCTT 1207
QY      68 CACCCCATGATGATAGCGGCGCAAGCTGCGCCCTGCTGCGGAAGCTGATGATGATGCG 127
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1208 CTTTCATCAGTGCATGCGCGCGGCTGCTGCGGCGCCCTTGTATTGACCATGCG 1267
QY      128 GCGTCGCTGCGCGGCGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1268 ACGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1327
QY      187 TGGCGTCCGCGGCGGCGGCGGATGAGGGCGGCACTGGGTGGTG 230
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1328 CCGCACGCGCGGTGGCGCGCGCAACATGACGTGACGCGGCGGCGGCG 1371

Search completed: December 26, 2002, 03:46:43
Job time : 386 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 22:44:43 ; Search time 2088 Seconds
(without alignments)
3816.178 Million cell updates/sec

Title: US-09-548-449-3

Perfect score: 492
Sequence: 1 actgcgcagcattcacc.....gccttaacctagcaagac 492

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hnc:*
9:	gb_estl:*
10:	gb_est2:*
11:	gb_hnc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estom:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vit:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.4	12.1	925	17	CNS0091P
2	53.6	10.9	1101	17	AL108460 Drosophila
3	51	10.4	152	12	CNS017SY
4	49.8	10.1	523	12	BC487612 EML_65_B1
5	48.8	9.9	610	10	BE266741 HV_CGA001
6	48.2	9.8	764	9	BE426427 WHE0335_H
					AL547921 AL547921

C	7	48	9.8	332	10	BE597437
C	8	47.6	9.7	130	12	BF485240
C	9	47.6	9.7	392	12	BG356596
C	10	47.6	9.7	529	10	AM678427
C	11	47.6	9.7	536	10	AM747229
C	12	47.6	9.7	587	10	AM680372
C	13	47.6	9.7	617	10	AM678141
C	14	47.4	9.6	803	17	AG162326
C	15	47.2	9.6	697	10	AM155495
C	16	47.2	9.6	920	10	AM155435
C	17	47.2	9.6	935	12	CNS006XK
C	18	47	9.6	497	17	BC366604
C	19	46.8	9.5	617	10	BE195746
C	20	46.8	9.5	840	17	AG043467
C	21	46.6	9.5	932	17	CNS00720
C	22	46.4	9.4	367	13	BM318362
C	23	46.4	9.4	571	10	AM672287
C	24	46.4	9.4	844	17	CNS0052P
C	25	46.2	9.4	631	9	AL508579
C	26	46	9.3	925	17	CNS0091P
C	27	46	9.3	1008	14	BO708747
C	28	46	9.3	1071	17	CNS00EMV
C	29	45.6	9.3	485	10	BE599458
C	30	45.6	9.3	488	13	BM376745
C	31	45.6	9.3	535	13	BM329587
C	32	45.6	9.3	558	14	BQ467551
C	33	45.6	9.3	561	12	BF619248
C	34	45.6	9.3	587	13	BM329864
C	35	45.6	9.3	632	12	BG708176
C	36	45.6	9.3	841	12	BF255640
C	37	45.6	9.3	848	12	BG310135
C	38	45.6	9.3	951	12	BG343611
C	39	45.6	9.3	993	12	BG343243
C	40	45.6	9.3	1219	14	BM803425
C	41	45.6	9.3	1511	14	BO900625
C	42	45.4	9.2	632	10	BE414408
C	43	45.4	9.2	736	14	BQ839017
C	44	45.2	9.2	338	13	BI306090
C	45	45.2	9.2	497	10	AM564083

ALIGNMENTS

RESULT 1
CNS0091P
LOCUS
DEFINITION
CNS0091P 925 bp DNA linear GSS 03-JUN-1999
BACR19D16 of RPCR-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
AL053013
VERSION
AL053013.1 GI:4934461
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster.
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 925)

AUTHORS
TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeawa and Aaron Mammoser in Pletier de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCR-98 and was constructed by partial

[illegible][illegible]

QY 103 GGGAAAGCTGTACATCTGATCGCGGCGGTGCGCGGGGCTTCCGCTCT 162
DB 304 GCGCGAGCTAGTGTGGATATGTGGCTCGATGCGCGGCGCGGCGGTGCGCTGCGCT 245
QY 163 GCGCGGTGCGGTCGCTGCGGCTTGGCGGCGCGGCGGCGGATGAGGCGGCGACT 222
DB 244 CGACGACGCGCACCAGGCTCTTCCAGGTGACATTGCGCGCGCCAGACTTGGGCGCG 185
QY 223 GGGTGTGATTCAGCCACTGAGCGTC 248
DB 184 GCGTCCGATACCCAGCGCGCGGCG 159

RESULT 14
AG162326 803 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-028L15.TU, genomic survey
DEFINITION
ACCESSION AG162326
VERSION AG162326.1 GI:16692004
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone: lib:RP43-43 Chimpanzee
ORGANISM Male BAC library clone: RP43-028L15.TU.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Tozaki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL BAC end sequences of library RPCR-43
AUTHORS Unpublished
2 (bases 1 to 803)
TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
JOURNAL Tozaki, Y., Watanabe, H. and Sakaki, Y.
AUTHORS Direct Submission
TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpesgsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/;
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCR-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU
LIBRARY
VECTOR : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 803
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-028L15.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCR-43 Chimpanzee Male BAC library"
BASE COUNT 56 a 243 c 456 g 15 t 33 others
ORIGIN

Query Match 9.6%; Score 47.4; DB 17; Length 803;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 111; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 4 CGCGATCAATCTTACCATCGGCGCACTCTCTGCGGATTCCTGCTCTCTCTCA 63
DB 725 CGCGGCG 666
QY 64 CGCGACCCCGCATGTAGCGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 123
DB 665 GCG 606

QY 124 GCGCGCGCTGCTGCTGCGCGCGCGCGGCTCTTCCGCTCTGCTGCGGCTCGGCG 183
DB 605 GCG 546
QY 184 CCGTGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 225
DB 545 CCG 504

RESULT 15
AM155496 697 bp mRNA linear EST 03-NOV-1999
LOCUS mg1e0026009f Rice blast infection stage cDNA library Oryza
DEFINITION sativa/Piricularia oryzae mixed EST library cDNA clone mg1e0026009f
, mRNA sequence.
ACCESSION AM155496
VERSION AM155496.1 GI:6224365
KEYWORDS EST.
SOURCE Oryza sativa/Piricularia oryzae mixed EST library.
ORGANISM Oryza sativa/Piricularia oryzae mixed EST library.
Eukaryota; mixed EST libraries.
REFERENCE
AUTHORS Rauyaree, P., Choi, W., Fang, E., Blackmon, B. and Dean, R.A.
TITLE Genes expressed during early stages of rice infection with the rice
JOURNAL blast fungus Magnaporthe oryzae
Mol. Plant Pathol. 2 (6), 347-354 (2001)
CONTACT: Dean, R.A.
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: r3 primer (AATTAACCTTCACATAAGG)
High quality sequence stop: 51.
Location/Qualifiers
1. 697
/organism="Oryza sativa/Piricularia oryzae mixed EST
library"
/strain="70-15"
/db_xref="taxon:105664"
/clone="mg1e0026009f"
/clone_lib="Rice blast infection stage cDNA library"
/dev_stage="Infection stage at 48 hour post-inoculation"
/note="Vector: pBluescriptII SK(+). Vector: Rice
blast-infected leaves at 48 hour post-inoculation mRNA for
cDNA library construction."
BASE COUNT 150 a 207 c 188 g 150 t 2 others
ORIGIN

Query Match 9.6%; Score 47.2; DB 10; Length 697;
Best Local Similarity 53.2%; Pred. No. 1.1;
Matches 100; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 75 ATGCTAGCGCGCAGCTGCGCGCGCTGCGGAAAGCTGATCTGATCGCGGCGTGC 134
DB 428 ATGCTGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 369
QY 135 GTGCGCGCGCGCGCGCGCTGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 194
DB 368 AGCAGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 309
QY 195 GCG 254
DB 308 GCGAGGAGCG 249
QY 255 CCAGTAC 262
DB 248 GCGACCAAC 241

Search completed: December 26, 2002, 08:15:22
Job time : 2112 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 20:22:07 ; Search time 56 Seconds
(without alignments)
2694.374 Million cell updates/sec

Title: US-09-548-449-3

Perfect score: 492
Sequence: 1 actcgcgcagcatcattccacc.....gccttaacctagcaagac 492

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/prodata1/1na/5B_COMB.seq: *
3: /cgn2_6/prodata1/1na/6A_COMB.seq: *
4: /cgn2_6/prodata1/1na/6B_COMB.seq: *
5: /cgn2_6/prodata1/1na/PCTUS_COMB.seq: *
6: /cgn2_6/prodata1/1na/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	45.6	9.3	530	3	US-08-758-662-4
2	45.6	9.3	4524	2	US-08-845-898-7
3	45.6	9.3	4524	3	US-09-206-537-7
4	45.6	9.3	4524	4	US-09-430-854-7
5	44.2	9.0	1146	1	US-08-482-385A-1
6	44.2	9.0	2728	1	US-08-482-385A-5
7	44.2	8.9	4257	2	US-08-690-473-1
8	44.2	8.9	4257	4	US-09-259-821A-1
9	44.2	8.9	4257	4	US-08-843-659-1
10	44.2	8.9	12001	1	US-08-458-568A-11
11	43.8	8.9	68750	3	US-09-335-409-1
12	43.8	8.9	68750	4	US-09-568-102-1
13	43.8	8.9	68750	4	US-09-567-969-1
14	43.8	8.9	68750	4	US-09-568-480-1
15	43.8	8.9	68750	4	US-09-568-486-1
16	43.8	8.9	68750	4	US-09-568-472-1
17	43.8	8.9	68750	4	US-09-567-899-1
18	43.8	8.9	71989	4	US-09-443-501A-2
19	42.8	8.7	367	4	US-09-072-596-249
20	42.8	8.7	1028	4	US-08-118-700-1
21	42.8	8.7	1028	4	US-08-458-745-1
22	42.4	8.6	2846	4	US-09-613-182-5
23	42.4	8.6	44377	2	US-08-804-227C-7
24	42.4	8.6	44377	2	US-08-804-198-1
25	42.2	8.6	1926	4	US-09-249-585A-4
26	42.2	8.6	1931	2	US-09-130-114-2
27	41.2	8.4	4403765	4	US-09-103-840A-2

C 28	41	8.3	861	2	US-08-924-759-15	Sequence 15, Appl
C 29	41	8.3	861	3	US-09-248-335-15	Sequence 15, Appl
C 30	41	8.3	1279	3	US-09-248-335-25	Sequence 25, Appl
C 31	40.8	8.3	2214	3	US-08-864-038A-1	Sequence 1, Appl
C 32	40.8	8.3	2889	3	US-08-537-002A-4	Sequence 4, Appl
C 33	40.8	8.3	2889	3	US-08-863-010-4	Sequence 4, Appl
C 34	40.8	8.3	3331	3	US-09-024-429-4	Sequence 4, Appl
C 35	40.8	8.3	3331	3	US-08-864-038A-2	Sequence 2, Appl
C 36	40.8	8.3	3600	1	US-08-864-038A-4	Sequence 4, Appl
C 37	40.8	8.3	3600	3	US-08-537-002A-5	Sequence 5, Appl
C 38	40.8	8.3	3600	4	US-08-863-010-5	Sequence 5, Appl
C 39	40.8	8.3	3600	4	US-09-024-429-5	Sequence 5, Appl
C 40	40.6	8.3	2185	1	US-08-173-508-3	Sequence 3, Appl
C 41	40.6	8.3	2185	2	US-08-265-310-3	Sequence 3, Appl
C 42	40.6	8.3	2185	2	US-08-951-742-3	Sequence 3, Appl
C 43	40.4	8.2	16442	3	US-08-781-891-208	Sequence 208, App
C 44	40.2	8.2	304	4	US-09-056-556-166	Sequence 166, App
C 45	40.2	8.2	304	4	US-09-072-596-161	Sequence 161, App

ALIGNMENTS

```
RESULT 1
US-08-758-662-4
; Sequence 4, Application US/08758662
; Patent No. 6114150
; GENERAL INFORMATION:
; APPLICANT: Weissman, Sherman
; APPLICANT: Baskaran, Namadev
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,662
; FILING DATE: 29-Nov-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6114150tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 390036.402C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-758-662-4
;
Query Match          9.3%  Score 45.6; DB 3; Length 530;
Best Local Similarity 54.3%  Pred. No. 0.057;
Matches 113; Conservative 0; Mismatches 94; Indels 1; Gaps 1;
QY 22 TCGGCGGCACTCGCGGGATATCTGCTCTCCACCGGACCCGCAATGCTAG 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 TGACACATCTCTCGCGCGCTCGGCTCGGCTCAGGCGGCGGCGGCGGCGG 323
QY 82 CGGCGACATCGCGCTCGGCGGAAAGCTTACATGCTG-ATGCGGCGGCTGCGG 140
    ||||| || || ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

[illegible]

RESULT 2

```

1Sequence 7, Application US/08845998
2Patent No. 5878892
3
4GENERAL INFORMATION:
5APPLICANT: Van Baren, Nicolas
6APPLICANT: Coultre, Pierre G.
7APPLICANT: De Smet, Charles
8APPLICANT: Lucas, Sophie
9APPLICANT: Boon, Thierry
10TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
11NUMBER OF SEQUENCES: 16
12CORRESPONDENCE ADDRESS:
13ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
14STREET: 600 Atlantic Avenue
15CITY: Boston
16STATE: MA
17COUNTRY: US
18ZIP: 02210
19COMPUTER READABLE FORM:
20MEDIUM TYPE: Floppy disk
21COMPUTER: IBM PC compatible
22OPERATING SYSTEM: PC-DOS/MS-DOS
23SOFTWARE: Patent Release #1.0, Version #1.25
24CURRENT APPLICATION DATA:
25APPLICATION NUMBER: US/08/845,998
26FILING DATE:
27CLASSIFICATION: 435
28ATTORNEY/AGENT INFORMATION:
29NAME: Van Amsterdam, John R.
30REGISTRATION NUMBER: 40,212
31REFERENCE/DOCKET NUMBER: L0461/7008
32TELECOMMUNICATION INFORMATION:
33TELEPHONE: (617)720-3500
34TELEFAX: (617)720-2441
35INFORMATION FOR SEQ ID NO: 7:
36SEQUENCE CHARACTERISTICS:
37LENGTH: 4524 base pairs
38TYPE: nucleic acid
39STRANDEDNESS: double
40TOPOLOGY: linear
41MOLECULE TYPE: cDNA
42HYPOTHEetical: NO
43ANTI-SENSE: NO
44FEATURE:
45NAME/KEY: CDS
46LOCATION: 174..1433
47US-08-845-998-7

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Query Match	9.38;	Score 45.6;	DB 2;	Length 4524;
Best Local Similarity	54.38;	Pred. No. 0.072;		
Matches 113; Conservative	0;	Mismatches 94;	Indels 1;	Gaps 1

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Db	523	TGGACCAATCTCTCGCGCGTCGTCCGCTCATATGGCCGGGGGGGGGGGGGG	582
QY	82	CGGCGAGTGGCGGCGCTGCGGGGAAGCTGTAAATCTG-ATCGGGGGCTCGGTCCG	140
Db	583	CGCGCGGCGGGCGGCGGCCACACAGCGCCCGGGGGGCGGTGGCGGCCCGGCGGGG	642
QY	141	CGGCGCGGATCTCGGCTGCTGGCGGATGCCGGTCCGATGGGACTTGGCGTCCGCGG	200

[illegible]

RESULT 3

Sequence 7, Application US/09206537
 Patent No. 6130052
 GENERAL INFORMATION:
 APPLICANT: Van Baren, Nicolas
 APPLICANT: Coulle, Pierre G.
 APPLICANT: De Smet, Charles
 APPLICANT: Lucas, Sophie
 APPLICANT: Boon, Thierry
 TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/206,537
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/845,998
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Van Amsterdam, John R.
 REGISTRATION NUMBER: 40,212
 REFERENCE/DOCKET NUMBER: L0461/7008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)720-3500
 TELEFAX: (617)720-2441
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4524 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 174..1433
 US-09-206-537-7

Query Match	9.38;	Score 45.6;	DB 3;	Length 4524;
Best Local Similarity	54.38;	Pred. No. 0.072;		
Matches 113;	Conservative 0;	Mismatches 94;	Indels 1;	Gaps 1

Qy	Db	Qy	Db	Qy	Db
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TCGGCCGCAATCTCTGGGGGATATCTCTGTCCTCTCACCGGCACTCCCATGGTAG	TGACACATCTCTTCGCGCGTCTCGCGCTCATAGGCGGAGGGGGGCGGGGCGG	CGCGCAGCTCGCGCCCTCCCTGGGAAAGCTATATCTGT-ATGAGGGGCGTGGTGGC	CGCGCAGCTCGCGCCCTCCCTGGGAAAGCTATATCTGT-ATGAGGGGCGTGGTGGC	CGCGCAGCTCGCGCCCTCCCTGGGAAAGCTATATCTGT-ATGAGGGGCGTGGTGGC	CGCGCAGCTCGCGCCCTCCCTGGGAAAGCTATATCTGT-ATGAGGGGCGTGGTGGC
CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG
64.2	58.2	64.2	58.2	64.2	58.2
CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG	CGCGCGGGGGCGGGCGCGCGCACACAGCGCCCCGGGGGGCGGGGGCGCGCGCGCG
200	582	200	582	200	582


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Patent No. 5728561
GENERAL INFORMATION:
APPLICANT: DENOVA,, CLAUDIO D.
TITLE OF INVENTION: GENES ENCODING BRANCHED CHAIN ALPHA
KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER C. RICHARDSON
STREET: 235 EAST 42ND STREET, 20TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A
ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,385A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHEYKA,, ROBERT F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC8346C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-573-1189
TELEFAX: 212-573-1939
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-482-385A-5

Query Match          9.0%, Score 44.2; DB 1; Length 2728;
Best Local Similarity 52.4%; Pred.No.0.14;
Matches   97; Conservative    0; Mismatches   88; Indels    0; Gaps    0;

QY      52 CCTGCTCCTCCACCGGGCACCCCAGTGTAGCGGGCCAGCTCGGCCCTGCTGGGAAGCT 111
DB      1204 CGCGCTTCACGAGCGCTCGGCCCCCTCCCGCGCGCGGTGGGCACAGGCGTGATGGA 1145
QY      112 GTACATGCTGATCGGCGGCGTGTGCGCGGCGGGGCTTCCGCTGCTCGGCGTGC 171
DB      1144 CCTGCTGCACGGGCGCGCCGCGCTGTGTCGCTGCACAGCGGCGCCGCACTCCGTACCGCA 1085
QY      172 CGGTCGTCGGGCGCTTGGCGCTCGCGCGGCGGCGCGCATGAGGCGGCGACACTGGGTGTGA 231
DB      1084 CGGCGCTGTGGGCGACGACGAGGCGGCGGCTGCTGCTGGCGAGCGGAGCGAGATGGCGCA 1025
QY      232 TCCAG 236
DB      1024 AGCGG 1020

RESULT 7
US-08-690-473-1/c
Sequence 1, Application US/08690473
Patent No. 5876923
GENERAL INFORMATION:
APPLICANT: Leopardl, Rosario
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
```

```

1 STATE: Texas
2 COUNTRY: USA
3 ZIP: 77210
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patentin Release #1.0, Version #1.30
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/690,473
12 FILING DATE: 26-JUL-1996
13 CLASSIFICATION: 435
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Highlander, Steven L.
16 REGISTRATION NUMBER: 37,642
17 REFERENCE/DOCKET NUMBER: AUCD:239
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 512/418-3000
20 TELEFAX: 512/474-7577
21 INFORMATION FOR SEQ ID NO: 1:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 4257 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27
28 US-08-690-473-1
29
30 Query Match 8.9%; Score 44; DB 2; Length 4257;
31 Best Local Similarity 50.5%; Pred. No. 0.16;
32 Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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34 QY 19 CGATGCGCCGCAACCTCCGCGGAGATATCTGCTCTCTCTCCCTCCACCGGACCCCAATGG 78
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36 Db 613 CCAGTGTGTCGGGCGAGACGGGCTCCCGCGCTCTCCGCGGCTGGGCGCCGCGG 554
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38 QY 79 TAGCGCGCAGCGTCGGGCGCCCTCGCTGGGAAGCTGTAACTGATCGGCGCGCTGCGTGC 138
39 |||||
40 Db 553 GGGCCCTCCGCTCCCGCGGCGCTGTGAGGTCTGGGGGTGTGTGCGGCTGTGTGTCGG 494
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42 QY 139 CGGCGCGCGGTCTTCGCGCTGCTGCGGCGTGCAGGTCCGTGCGGCGCTTGCGTCCGCG 198
43 |||||
44 Db 493 GGTGCTCCCGCGCTCTCGTGTGTCGCGGCGCCCGACCGGAGGCGCCCGCGTGTGCGGT 434
45
46 QY 199 CGGCGCGCATGAGGCGCGCACCTGGGTGCTG 230
47 |||||
48 Db 433 CTGGGCTCGGGGTGGGCGGCGCGCTGCGGTG 402
49
50 RESULT 8
51 US-09-259-821A-1/c
52 ; Sequence 1, Application US/09259821A
53 ; Patent No. 6210926
54 ; GENERAL INFORMATION:
55 ; APPLICANT: LEOPARDI, ROSARIO
56 ; APPLICANT: ROIZMAN, BERNARD
57 ; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICp4 IS AN INHIBITOR OF APOPTOSIS
58 ; FILE REFERENCE: AUCD:317
59 ; CURRENT APPLICATION NUMBER: US/09/259,821A
60 ; CURRENT FILING DATE: 1999-03-01
61 ; PRIOR APPLICATION NUMBER: 08/690,473
62 ; PRIOR FILING DATE: 1996-07-26
63 ; NUMBER OF SEQ ID NOS: 2
64 ; SOFTWARE: Patentin Ver. 2.1
65 ; SEQ ID NO 1
66 ; LENGTH: 4257
67 ; TYPE: DNA
68 ; ORGANISM: HERPES VIRUS, TYPE 1
69 US-09-259-821A-1
70
71 Query Match 8.9%; Score 44; DB 4; Length 4257;
72 Best Local Similarity 50.5%; Pred. No. 0.16;
73 Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Db 613 CCAGCTGTGCGGCGAGACGCTCCCGGCTCTGCGGCGGTGGTGCCCGCGG 554
QY 79 TAGCGGCACAGTCGCGCCCTGCTGGAAAGCTACATGCTGATGCGGCGCTCGGTG 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 GGGCCCTCCCGTCCCGCGGCGCTCTGAGGCTGTGGGGGTGTGGGGTCTGTGGTGG 494
QY 139 CGGCGCGCGGCTCTGCGGCTGCTGCGGCGGTGCGGCTGCGGCGCTGCGCGG 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 GGTGTGTCGGCGGCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 434
QY 199 CGGCGCGCGATGAGCGCGGCGGCTGCTG 230
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Db 433 CTGGGCTCGGGGTGGGCGGCGGCGGCGGCTCGGTG 402

RESULT 9
US-08-843-659-1/C
; Sequence 1, Application US/08843659
; Patent No. 6218103
; GENERAL INFORMATION:
; APPLICANT: Leopardi, Roarlio
; APPLICANT: Roizman, Bernard
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,659
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:519
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-843-659-1

Query Match 8.9%; Score 44; DB 4; Length 4257;
Best Local Similarity 50.5%; Pred. No. 0.16;
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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QY 199 CGGCGCGCGATGAGCGCGGCACTGGGTGTG 230
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Db 433 CTGGGCTCGGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 402

RESULT 10
US-08-458-568A-11
; Sequence 11, Application US/08458568A
; Patent No. 5821339
; GENERAL INFORMATION:
; APPLICANT: Schaffer, Priscilla A.
; APPLICANT: Ieh, Lily
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
; TITLE OF INVENTION: Infections
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpes simplex virus
; STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11

Query Match 8.9%; Score 44; DB 1; Length 12001;
Best Local Similarity 50.5%; Pred. No. 0.18;
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 22:45:58 ; Search time 236 Seconds

(without alignments)
846.895 Million cell updates/sec

Title: US-09-548-449-3

Perfect score: 492
Sequence: 1 actcgcgatcatctacc.....gccttaactagaagac 492

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45.6	9.3	530	US-10-073-353-4	Sequence 4, Appli
2	44.4	8.9	4257	US-09-825-288A-1	Sequence 1, Appli
3	43.8	8.9	68750	US-10-014-717-1	Sequence 1, Appli
4	43.4	8.8	1131	US-09-712-363-93	Sequence 93, Appli
5	43.4	8.8	1305	US-09-815-242-7730	Sequence 727, Ap
6	41.8	8.5	1360	US-09-867-550-1927	Sequence 1927, Ap
7	41.1	8.3	1665	US-09-815-242-7935	Sequence 7935, Ap
8	40.2	8.2	1428	US-09-921-332-5	Sequence 5, Appli
9	40.2	8.2	1428	US-09-921-330-5	Sequence 5, Appli
10	40.2	8.2	1428	US-09-921-329-5	Sequence 5, Appli
11	40.2	8.2	2481	US-09-894-998-35	Sequence 35, Appli
12	39.6	8.0	4446	US-09-815-242-7983	Sequence 7983, Ap
13	39.4	8.0	550	US-09-791-171-63	Sequence 63, Appli
14	39.4	8.0	2561	US-09-976-740-48	Sequence 48, Appli
15	39.4	8.0	2561	US-10-023-529-48	Sequence 48, Appli
16	39.4	8.0	2561	US-10-023-523-48	Sequence 48, Appli
17	39.4	8.0	3032	US-09-954-1043-1	Sequence 1, Appli
18	39.4	8.0	3152	US-09-880-107-3431	Sequence 3431, Ap
19	39.2	8.0	1771	US-09-991-436-7	Sequence 7, Appli

C 20	39.2	8.0	1771	10	US-09-874-923-7	Sequence 7, Appli
C 21	39	7.9	684	10	US-09-969-708-52	Sequence 52, Appli
C 22	39	7.9	684	10	US-09-880-107-1604	Sequence 1604, Ap
C 23	38.8	7.9	4039	10	US-09-205-448-7	Sequence 7, Appli
C 24	38.6	7.8	1436	10	US-09-788-345-11	Sequence 11, Appli
C 25	38.6	7.8	1518	10	US-09-815-242-7829	Sequence 7829, Ap
C 26	38.6	7.8	7419	10	US-09-815-242-4009	Sequence 4009, Ap
C 27	38.4	7.8	424	10	US-09-960-352-14599	Sequence 14599, A
C 28	38.4	7.8	429	9	US-09-854-133-413	Sequence 413, App
C 29	38.4	7.8	429	10	US-09-798-973-113	Sequence 413, App
C 30	38.4	7.8	1406	10	US-09-745-763-18	Sequence 18, Appli
C 31	38.4	7.8	3624	10	US-09-927-112-3	Sequence 3, Appli
C 32	38.4	7.8	4635	10	US-09-927-112-3	Sequence 3, Appli
C 33	38.4	7.8	4635	10	US-10-001-873-22	Sequence 22, Appli
C 34	38	7.7	1508	9	US-09-931-457A-61	Sequence 61, Appli
C 35	38	7.7	2162	10	US-09-799-875-10	Sequence 10, Appli
C 36	38	7.7	2586	9	US-09-905-291A-235	Sequence 235, App
C 37	38	7.7	2586	9	US-10-063-547-7	Sequence 7, Appli
C 38	38	7.7	2586	9	US-09-902-853-235	Sequence 235, App
C 39	38	7.7	2586	10	US-09-909-320-235	Sequence 235, App
C 40	38	7.7	2586	10	US-09-909-088B-235	Sequence 235, App
C 41	38	7.7	2586	12	US-10-006-667-7	Sequence 7, Appli
C 42	37.8	7.7	8509	10	US-09-826-205-1	Sequence 1, Appli
C 43	37.4	7.6	371	10	US-09-867-550-299	Sequence 299, App
C 44	37.4	7.6	3042	9	US-09-712-363-68	Sequence 68, Appli
C 45	37.4	7.6	3203	10	US-09-880-107-2164	Sequence 2164, Ap

ALIGNMENTS

RESULT 1
US-10-073-353-4
Sequence 4, Application US/10073353
Patent No. US2002016858A1

GENERAL INFORMATION:

APPLICANT: Sherman M. Weissman

Namadev Baskaran

TITLE OF INVENTION: Amplification of Nucleic Acids

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan, Lewis & Bockius LLP

STREET: 1111 Pennsylvania Ave., NW

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0. Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/073,353

FILING DATE: 03-May-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/758,662

FILING DATE: 1996-12-07

APPLICATION NUMBER: US 08/758,662 (CPA)

FILING DATE: 1999-02-17

ATTORNEY/AGENT INFORMATION:

NAME: Michael S. Tuscan

REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5007-03-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-739-3001

TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 base pairs

TYPE: nucleic acid

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: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-073-353-4

Query Match          9.3%; Score 45.6; DB 9; Length 530;
Best Local Similarity 54.3%; Pred. No. 0.0049;
Matches 113; Conservative 0; Mismatches 94; Indels 1; Gaps 1

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DB 264 TCGACCAATCTCTCTCTCGCGCTCGCTCGCTATGAGCGCGCGCGCGCGCGCGCGCG 323
OY 82 CGGCGAGCTCGCGCCCTCGCTGCGGAAGCTGACATGCTG-ATCGAGCGGCTGCGTCCG 140
DB 324 CGCGCGGGGGCGCGCGCGCGCCCGACAGCGCGCGGGGGCGCGGTGCGCGCGCGCGCG 383
OY 141 GCGCGCGGGCTTTCGCGCTGCTCGCGCGGTGCGGTGCGCGCTTGGCGTCCGCGCG 200
DB 384 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 443
OY 201 GCGCGCGATGAGCGCGCACTCGGGGTG 228
DB 444 GCGCGCGCGCGCGCGCGCTCTGCGCGG 471

RESULT 2
US-09-825-288A-1/c
: Sequence 1, Application US/09825288A
: Publication No. US20020192822A1
: GENERAL INFORMATION:
: APPLICANT: LEOPARDI, ROSARIO
: APPLICANT: ROTZMAN, BERNARD
: TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
: FILE REFERENCE: ARCD:317USCI
: CURRENT APPLICATION NUMBER: US/09/825,288A
: CURRENT FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: 09/259,821
: PRIOR FILING DATE: 1999-03-01
: PRIOR APPLICATION NUMBER: 08/690,473
: PRIOR FILING DATE: 1996-07-26
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 4257
: TYPE: DNA
: ORGANISM: HERPES VIRUS, TYPE 1
US-09-825-288A-1

Query Match          8.9%; Score 44; DB 9; Length 4257;
Best Local Similarity 50.5%; Pred. No. 0.021;
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0

OY 19 CCATGCGCGCAACTCTGCGGGATATCTCTCTCTCTCTCAACCGGACCCCATAG 78
DB 613 CCAGCTGTGCGGCGAGACGCGCTCCCGGCGTCTCTGCGCGCGTGGGCCCGCGCG 554
OY 79 TAGCGCGCACTCGCGCCCTGCTGCGGAAGCTGTACATGCTGATGCGCGCGCTGCTC 138
DB 553 GGGCGCTCCCGTCCCGCGCGGGGTGTGAGGTGTGCGGGGTGTGCGGGGTGCGG 494
OY 139 CGGCGCGCGGCTTTCGCTGCTGCGCGGTGCGCGGTGCGCGCTTGGCGTCCGCGG 198
DB 493 GGTGTCCCGCGCTCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434
OY 199 GCGCGCGGATGAGCGCGGCGACCTGGGTG 230
DB 433 CTGGCGCTGCGGGGTGGCGCGCGCGCGCGCGGTG 402

RESULT 3
US-10-014-717-1
: Sequence 1, Application US/10014717

```

```

? Publication No. US2002019278A1
? GENERAL INFORMATION:
? APPLICANT: Schupp, Thomas
? APPLICANT: Ligon, James
? APPLICANT: Molnar, Istvan
? APPLICANT: Zirkle, Ross
? APPLICANT: Cyr, Devon
? APPLICANT: Goerlach, Joern
? TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOPHILONES
? FILE REFERENCE: 4-30582A
? CURRENT APPLICATION NUMBER: US/10/014,717
? PRIOR FILING DATE: 2001-11-13
? PRIOR APPLICATION NUMBER: US/09/335,409
? PRIOR FILING DATE: 1999-06-17
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 68750
? TYPE: DNA
? ORGANISM: Sorangium cellulosum
US-10-014-717-1

Query Match          8.9%; Score 43.8; DB 9; Length 68750;
Best Local Similarity 52.5%; Freq. No. 0.046;
Matches    96; Conservative   0; Mismatches  87; Indels   0; Gaps   0.

OY      14 CTTCCACATTCGGCGGCCCAACTCCTGCGGGGATATCTGCCTCTCCCTCACCGCACCCC 73
Db 63905 CTCACCGAGCGCGCAGAGTTCGTGTCTGCCTGCTGCCTGCGCCCTCGCCTGTCTCTGAACCGCG 63964

OY      74 CATGTAGCGCGGCACCTGCGCGCCCTGCTGGGAAAGCTGTACATGTGATCGCGCGCTC 133
Db 63965 CGCGCCTTGCGGAGCATCGCGCGCGGCGCTGCCACAGCCCGAGAGCTCTCGCGCAGCTCTTC 64024

OY      134 GCTGCGCGCGCGCGCGGTCTTCGCCCTCTGCCTGCGCGGCGGCGGCGGCGCGGACCTTGAGCGCTC 193
Db 64025 GGCGCGCTGGTGCTGTGGGCCCGCTCGTCGTGCGCGCGCGCTGCCTCTCTGCTTCCATGAGTIC 64084

OY      194 CGC 196
Db 64085 CTC 64087

RESULT 4
US-09-712-363-93
? Sequence 93, Application US/09712363
? Patent No. US20020164588A1
? GENERAL INFORMATION:
? APPLICANT: Eisenberg, David
? APPLICANT: Rotstein, Sergio H.
? APPLICANT: Marcotte, Edward M.
? TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
? FILE REFERENCE: 07419-032001
? CURRENT APPLICATION NUMBER: US/09/712,363
? CURRENT FILING DATE: 2000-11-13
? PRIOR APPLICATION NUMBER: PCT/US00/02246
? PRIOR FILING DATE: 2000-01-28
? PRIOR APPLICATION NUMBER: 60/179,531
? PRIOR FILING DATE: 2000-02-01
? PRIOR APPLICATION NUMBER: 60/117,844
? PRIOR FILING DATE: 1999-01-29
? PRIOR APPLICATION NUMBER: 60/118,206,
? PRIOR FILING DATE: 1999-02-01
? PRIOR APPLICATION NUMBER: 60/126,593
? PRIOR FILING DATE: 1999-03-26
? PRIOR APPLICATION NUMBER: 60/134,093
? PRIOR FILING DATE: 1999-05-14
? PRIOR APPLICATION NUMBER: 60/134,092
? PRIOR FILING DATE: 1999-05-14
? PRIOR APPLICATION NUMBER: 60/165,124
? PRIOR FILING DATE: 1999-11-12
? PRIOR APPLICATION NUMBER: 60/165,086

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;; PRIOR FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 292
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 93
;; LENGTH: 1131
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-93

Query Match 8.8%; Score 43.4; DB 9; Length 1131;
Best Local Similarity 60.7%; Pred. No. 0.022;
Matches 71; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 112 GTACATCTGATCGCGCGCTGCGCGCGGCTCTTCGCGCTGCGCGCTGC 171
Db 650 GTACTGCGCGCATGCGCGCAAGTGGCGCGCTGTGGCGCGCGCGCGCTGC 709
QY 172 CGGTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 228
Db 710 CGGTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGC 766

RESULT 5

US-09-815-242-7730
; Sequence 7730, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7730
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1305)
US-09-815-242-7730

Query Match 8.8%; Score 43.4; DB 10; Length 1305;
Best Local Similarity 49.8%; Pred. No. 0.022;
Matches 110; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 4 CGCGATCCTTCACATCTCGCGCGCAACTCTCGCGGATATCTCTCTCTCTCA 63
Db 630 CGCGAAGACATGACATGCGCGCGCGCTCTGCGGACATCCCGCGATATCTCA 689

QY 64 CCGGACCCCATGTGTACGCGGACCTGCGGCTTGGGAAAGCTGTACATCTGAT 123
Db 690 CACCATCTGTGCGGAGAACCTCAAGAAATGAGTGGGTGAAGAGCTGTCCCGACG 749
QY 124 CGCGCGCTGCGGTGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 183
Db 750 CAGCGCTACTGACGCTCTACGACACACACGCGCTGCTGCGCGCGCGCTGCTGCG 809
QY 184 CTTGGCTCG 224
Db 810 CCATGCGCTGACACCTGTGCGGACGCGGAAATGCGCGCGCGCGCGCGCG 850

RESULT 6

US-09-867-550-1927/c
; Sequence 1927, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehrabian, Fud,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells a
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US9N 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1927
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1927

Query Match 8.5%; Score 41.8; DB 10; Length 1360;
Best Local Similarity 57.1%; Pred. No. 0.058;
Matches 76; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 84 GCCACTGCGCGCTGCTGCGGAAAGCTGTACATCTGTATGCGCGCGCTGCGCG 143
Db 140 GCATCTGAGACGACGCGCTGCTGCCCAACAAAGATGCGCGCGCGCGCGCTCG 81
QY 144 GCCGCTCTCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 203
Db 80 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 21
QY 204 CGCGATGAGCGCG 216
Db 20 CGCCTCCAGGCGG 8

RESULT 7

US-09-815-242-7935/c
; Sequence 7935, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

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RESULT 8
US-09-921-232--5/c
; Sequence 5, Application US/09921232
; Patent No. US20020102681A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; TITLE OF INVENTION: Metabolism In Plants
; FILE REFERENCE: 0706d4
; CURRENT APPLICATION NUMBER: US/09/921,232
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 09/677,064
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS

```

Query Match	8.2%	Score 40.2	DB 10	Length 1428
Best Local Similarity	49.3%	Pred. No. 0.15		
Matches 105	Conservative 0	Mismatches 108	Indels 0	Gaps 0
QY	13	TCCTCACCATCGGCGCGCAACTCTCTCGGGAAATCTCTCTCCCTCTCTCCACCGGACACC	72	
Db	298	TCCTCGGGAGCGCCCGCGGAGCTTTGGCTGTGAGAACCTCTTGGCTCTTCTTCGTGTGAGG	239	
QY	73	CCATGTAGCGGCGCCAGCTCGCGCCCTTGCCTGTGGGAAAGCTGTACATGCTGATCGGCGCT	132	
Db	238	CGTACCCACACGACACTCCCGGGGGAGGCGCGGACACACCGGCTCTCTCGGGGCT	179	
QY	133	CGGTGCGGCGCGCGCGGCTTTCGCGCTCTCTCGGCGGTGCGGTCCTCGGTGCGGCTTTGGCGT	192	
Db	178	CCGAGGAGCGCGCGCGGCGGTCTCGGCTCCCTCTCGTCCACGACCGCGCGACACCA	119	

; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 2561
 ; TYPE: DNA
 ; ORGANISM: Oryctolagus cuniculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (246)...(1895)
 US-10-023-529-48

Query Match 8.0%; Score 39.4; DB 12; Length 2561;
 Best Local Similarity 57.2%; Pred. No. 0.28;
 Matches 91; Conservative 0; Mismatches 66; Indels 2; Gaps 1;

QY 49 CGTCTCTCTCCACCGGACCCCATGTAAGCGGCCAGCTCGGCGCCCTGCTGGGAAA 108
 Db 1032 CTTCCTCGAGGCTACAGGCGCCGCGCGCCGCGCGCCGCGCCCTTCGCGCG 973
 QY 109 GCTGTACATGCTGATCGGCGGCGTGCAGCGCGCGCGCGCGCTTCGCGCCCTGCTGGGCGG 168
 Db 972 GCGGCTGTGGCTG--CTGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGCTGTGGCGG 915
 QY 169 TGCCGATCCGTCGCGCCTTGGCGTCCGCGCGCGCGCGCG 207
 Db 914 CGCCGCGGCGCTGTGCGGCGGCGGAGGCGGCACTCCCG 876

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 03:47:00 ; Search time 264 Seconds

(without alignments)
110.894 Million cell updates/sec

Title: US-09-548-449-8

Perfect score: 13

Sequence: 1 aatcaannatta 13

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	76.9	13	AAA95512	Consensus IHF bind
2	10	76.9	13	ABA2585	IHF binding site c
3	10	76.9	13	ABC22980	Oligonucleotide SE
4	10	76.9	13	ABC22981	Oligonucleotide SE
5	10	76.9	13	ABC22982	Oligonucleotide SE
6	10	76.9	13	ABC22983	Oligonucleotide SE
7	10	76.9	13	ABF44524	Oligonucleotide SE
8	10	76.9	13	ABF44525	Oligonucleotide SE
9	10	76.9	13	ABF44526	Oligonucleotide SE

10	10	76.9	13	23	ABF44527	Oligonucleotide SE
C 11	10	76.9	13	23	ABH60452	Oligonucleotide SE
12	10	76.9	13	23	ABH60453	Oligonucleotide SE
C 13	10	76.9	13	23	ABH60454	Oligonucleotide SE
C 14	10	76.9	13	23	ABH60455	Oligonucleotide SE
C 15	10	76.9	18	20	AAA22841	Oligonucleotide SE
16	10	76.9	19	21	AAA85862	Integrin subunit b
17	10	76.9	19	21	AAH61024	Cyclin B1 ribozyme
18	10	76.9	24	22	AAH33589	Forward PCR primer
19	10	76.9	26	24	ABN89968	Real-time validati
C 20	10	76.9	28	22	AAH2012	E. coli K123 tpia
C 21	10	76.9	28	22	AAH28565	tpia gene PCR prim
C 22	10	76.9	29	24	ABN99540	Fungal PCR primer S
C 23	10	76.9	29	24	ABK29137	Paecilomyces vario
C 24	10	76.9	36	19	AAV09780	Tobacco PABP probe
C 25	10	76.9	36	19	AAV09780	Tobacco PABP probe
C 26	10	76.9	43	19	AAV09787	Tobacco PABP Ksal
C 27	10	76.9	50	20	AAH52183	Synthetic plasmid
C 28	10	76.9	50	20	AAH52050	Synthetic plasmid
C 29	10	76.9	50	22	AAH79643	Human DNA contain
C 30	10	76.9	51	22	AAH79644	Human DNA contain
C 31	10	76.9	51	22	AAH32103	Human SNP oligonuc
C 32	10	76.9	53	24	ABA92528	Leucine zipper-hum
C 33	10	76.9	60	24	ABN41535	Human spliced tran
C 34	10	76.9	62	22	AAH24562	Human ovarian PCR-
C 35	10	76.9	78	16	AAH19807	Human gene signatu
C 36	10	76.9	87	22	AAH23585	Tetracycline promo
C 37	10	76.9	87	24	AAH34618	HBV infection regu
C 38	10	76.9	89	18	AAV77658	Staphylococcus aur
C 39	10	76.9	96	14	AAH41243	3'-5' m1cF RNA str
C 40	10	76.9	97	21	AAH17769	Human secreted pro
C 41	10	76.9	100	15	AAH2573	Candida albicans-s
C 42	9.6	73.8	13	23	ABF19650	Oligonucleotide SE
C 43	9.6	73.8	13	23	ABF19651	Oligonucleotide SE
C 44	9.6	73.8	13	23	ABF19652	Oligonucleotide SE
C 45	9.6	73.8	13	23	ABF19653	Oligonucleotide SE

ALIGNMENTS

RESULT 1
AAA95512
ID AAA95512 standard; DNA: 13 BP.
AC AAA95512;
XX
XX 27-FEB-2001 (first entry)
XX
XX Consensus IHF binding site.
DE
XX
XX Bacteria: infection; drug-resistant pathogen; cancer; typhoid fever;
KW bacterial meningitis; tuberculosis; antisense strand; ribozyme;
KW toxic protein; ds.
XX
XX Unidentified.
OS
XX
XX W0200061804-A1.
XX
XX 19-OCT-2000.
XX
XX 14-APR-2000; 2000WO-US10229.
XX
XX 14-APR-1999; 99US-0291902.
PR 13-APR-2000; 2000US-0548449.
XX
XX (MUSC-) MUSC FOUND RES DEV.
PA (MUSC-) UNIV PENN STATE.
XX
XX Norris J, Clawson G, Westwater C, Schofield D, Schmidt M, Hoel B;
PI Dolan J, Pan W;
XX
XX WPI; 2000-638570/61.

XX New recombinant nucleic acid comprising a nucleotide sequence encoding
PT one or more toxic agents operably linked to a pathogen specific or
PT tissue specific promoter is useful for inhibiting replication of a
PT pathogen -
XX
PS Example: Page 67; 113pp; English.
XX
CC The present sequence comprises the consensus IHF binding site, which
CC was used in the construction of the pathogen and tissue-specific toxic
CC agents of the invention. These agents may be antisense sequences,
CC ribozymes or toxic proteins. These can be used in the treatment of cancer
CC and infections including hepatitis, herpes, malaria, bacterial
CC meningitis, typhoid fever and tuberculosis.
XX
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 3 T; 3 other;
XX
Query Match 76.9%; Score 10; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AATCAANNNTTA 13
DB 1 AATCAANNNTTA 13
IIIIIIIIII
RESULT 2
ABA02585 standard; DNA; 13 BP.
XX ABA02585;
XX
AC ABA02585;
XX
DT 05-FEB-2002 (first entry)
XX
XX IHF binding site consensus sequence.
XX
DE Infection; antisense RNA; ribozyme; antiviral; gene therapy;
XX papilloma virus; hepatitis B virus; cytotoxic; cytostatic; wart;
XX cervical dysplasia; cervical carcinoma; carcinoma; laryngeal papilloma;
XX IHF binding site; ss.
XX
OS Synthetic.
XX
XX WO200179524-A2.
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US12130.
XX
XX 13-APR-2000; 2000US-0548449.
XX
XX 07-DEC-2000; 2000US-251810P.
XX
XX (UYSC-) UNIV SOUTH CAROLINA.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX
XX Norris JS, Clawson GA, Westwater C, Schofield D, Schmidt MG;
XX Hoel B, Dolan J, Pan W;
XX
XX WPI; 2001-607700/69.
XX
XX Novel nucleic acid for the treatment of papilloma or hepatitis virus
XX induced conditions comprises a catalytic region which produces a
XX cytotoxic or cytostatic effect in the infected cell -
XX
XX Examples: Page 79; 143pp; English.
XX
CC The invention relates to the discovery, identification and
CC characterisation of toxic agents lethal to pathogens and methods for
CC targeting such toxic agents to a pathogen or pathogen infected cells in
CC order to treat and/or eradicate the infection. In particular the
CC invention relates to at least one nucleic acid molecule, which
CC specifically hybridises to mRNA encoding at least one viral protein
CC associated with the transformation or plasmid copy number control, which

CC hybridises to a viral polyadenylation signal or a core, pre core or
CC polymerase encoding sequence. Specifically, the invention relates to the
CC delivery of one or more toxic gene products, antisense RNAs, ribozymes,
CC DNAzymes or a combination thereof. The nucleic acids have antiviral
CC activity and can be used in gene therapy. They are useful for the
CC treatment of papilloma or hepatitis virus induced conditions and can
CC produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis B
CC infected cells. The papilloma virus induced condition is selected from
CC warts, cervical dysplasia, cervical carcinoma, carcinoma in situ and
CC laryngeal papilloma. The present sequence is that of the IHF binding
CC site consensus sequence featured in the bacteriophage P1 pac site
CC sequence (ABA02577).
XX
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 3 T; 3 other;
XX
Query Match 76.9%; Score 10; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AATCAANNNTTA 13
DB 1 AATCAANNNTTA 13
IIIIIIIIII
RESULT 3
ABC22980/C
ID ABC22980 standard; DNA; 13 BP.
XX ABC22980;
XX
AC ABC22980;
XX
DT 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 22997 for detecting SNP TSC0004518.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 22997; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABR00010-ABR99989 and
XX AB100010-AB182073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 other;

Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13
13 AATCAATAACTTA 1

RESULT 4

ABC22981
ID ABC22981 standard; DNA; 13 BP.

AC ABC22981;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 22998 for detecting SNP TSC0004518.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

PT WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

PS Claim 1; SEQ ID 22998; 29pp + Sequence Listing: German.

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC AB100010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 other;

Query Match 76.9%; Score 10; DB 23; Length 13;

Best Local Similarity 76.9%; Pred. No. 1.1e+04;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13

13 AATCAATAACTTA 13

RESULT 5

ABC22982/c

ID ABC22982 standard; DNA; 13 BP.

AC ABC22982;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 22999 for detecting SNP TSC0004518.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

PT WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

PS Claim 1; SEQ ID 22999; 29pp + Sequence Listing: German.

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC AB100010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;

Query Match 76.9%; Score 10; DB 23; Length 13;

Best Local Similarity 76.9%; Pred. No. 1.1e+04;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13

13 AATCAATAACTTA 1

RESULT 6

ABC22983

```
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 23000; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system and metabolic disorders. The
XX central nervous system, cardiovascular and gastrointestinal, respiratory,
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABIO0010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
XX
SQ
XX
XX Query Match 76.9%; Score 10; DB 23; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.1e+04;
XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 AATCAANNANTTA 13
XX ||||| | |||
XX 1 AATCAAAACTTA 13
XX
XX
XX RESULT 7
XX ABF44524/C
XX ID ABF44524 standard; DNA; 13 BP.
XX
XX ABF44524;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 144521 for detecting SNP TSC0036340.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
```

```
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 144521; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABIO0010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;
XX
SQ
XX
XX Query Match 76.9%; Score 10; DB 23; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.1e+04;
XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 AATCAANNANTTA 13
XX ||||| | |||
XX 13 AATCAATAATTA 1
XX
XX
XX RESULT 8
XX ABF44525
XX ID ABF44525 standard; DNA; 13 BP.
XX
XX ABF44525;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 144522 for detecting SNP TSC0036340.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 144522; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
```


CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABH99989 and
CC AB100010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
Db 1 AATCAATTAATAATTA 13
|||||
RESULT 9
ABF44526/c
ID ABF44526 standard; DNA; 13 BP.
XX
AC ABF44526;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144523 for detecting SNP TSC0036340.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN W0200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-1B00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PS Claim 1; SEQ ID 144523; 29pp + Sequence listing; German.
XX
SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
Db 13 AATCAACAAATTA 1
|||||
RESULT 10
ABF44527
ID ABF44527 standard; DNA; 13 BP.
XX
AC ABF44527;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144524 for detecting SNP TSC0036340.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN W0200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-1B00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PS Claim 1; SEQ ID 144524; 29pp + Sequence listing; German.
XX
SQ Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
Db 1 AATCAACAAATTA 13
|||||
RESULT 11
ABH60452/c
ID ABH60452 standard; DNA; 13 BP.
XX
AC ABH60452;
XX
DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 260429 for detecting SNP TSC0063245.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-1B00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI: 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1: SEQ ID 260429; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
SQ
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 AATCAANNANTTA 13
DB 13 AATCAANNANTTA 1
RESULT 12
ABH60453
ID ABH60453 standard: DNA; 13 BP.
XX
XX ABH60453;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 260430 for detecting SNP TSC0063245.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX

PF 06-APR-2001; 2001WO-1B00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI: 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1: SEQ ID 260430; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
SQ
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 AATCAANNANTTA 13
DB 1 AATCAANNANTTA 13
RESULT 13
ABH60454/C
ID ABH60454 standard: DNA; 13 BP.
XX
XX ABH60454;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 260431 for detecting SNP TSC0063245.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-1B00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI: 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PT

XX Claim 1; SEQ ID 260431; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC AB000010-AB099989, AB000010-AB099989, AB000010-AB099989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 other;
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
13 AATCAACTATTTA 1
DE
RESULT 14
ABH60455
ID ABH60455 standard; DNA; 13 BP.
AC ABH60455;
XX
XX 22-FEB-2002 (first entry)
DE
XX Oligonucleotide SEQ ID NO 260432 for detecting SNP TSC0063245.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status
XX
XX Claim 1; SEQ ID 260432; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and
XX AB100010-AB182073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 other;
Query Match 76.9%; Score 10; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
1 AATCAACTATTTA 13
DE
RESULT 15
AAA22841/C
ID AAA22841 standard; RNA; 18 BP.
AC AAA22841;
XX
XX 19-JUN-2000 (first entry)
DE
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6067.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tubercous sclerosis; pct-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US06507.
XX
XX 27-MAR-1998; 98US-0079678.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Payco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or
XX stability of an mRNA encoding an angiogenic factors
XX
XX Claim 54; Page 245; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with
XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a TIE-2 gene. AA16775 to
XX AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
XX and AA17168 to AA17560 and AA17623 to AA17684 represent their
XX corresponding target sequences; AA17685 to AA18385 and AA19087 to
XX AA19154 represent ribozyme sequences for TIE-2, and AA18386 to AA19086
XX and AA19155 to AA19222 represent their corresponding target sequences;
XX AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
XX AA21596 to AA21688 represent their corresponding target sequences;
XX AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
XX AA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX Integrin subunit beta 3, integrin subunit alpha 6, or TIE-2. They are

CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (AMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or Integrin subunit beta-3.

XX Sequence 18 BP; 4 A; 1 C; 1 G; 12 U; 0 other;

Query Match 76.9%; Score 10; DB 20; Length 18;
 Best Local Similarity 76.9%; Pred. No. 1.1e+04;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNANTTA 13
 ||||| |
 Db 14 AATCAAAAAATTA 2

Search completed: December 26, 2002, 08:24:21
 Job time : 271 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 08:15:31 ; Search time 1969 Seconds
(without alignments)
106.928 Million cell updates/sec

Title: US-09-548-449-8
Perfect score: 13
Sequence: 1 aatcaannantta 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	76.9	21	9	AU258344
2	10	76.9	29	17	BH854703
3	10	76.9	31	17	AZ837501
4	10	76.9	34	17	BH854706
5	10	76.9	35	17	AZ439152
6	10	76.9	36	17	BH854728

C 7	10	76.9	37	17	BH854701	BH854701	SALK_0889
C 8	10	76.9	37	17	BH854911	BH854911	SALK_0872
C 9	10	76.9	46	17	AZ359655	AZ359655	1M0102A08
C 10	10	76.9	46	17	AZ508716	AZ508716	1M0351114
C 11	10	76.9	47	17	AZ481968	AZ481968	1M0306110
C 12	10	76.9	49	10	AV856952	AV856952	AV856952
C 13	10	76.9	49	10	BH810378	BH810378	SALK_0492
C 14	10	76.9	49	17	BH861490	BH861490	SALK_0816
C 15	10	76.9	51	9	AU257483	AU257483	AU257483
C 16	10	76.9	51	17	BH791803	BH791803	SALK_0614
C 17	10	76.9	52	9	AU060328	AU060328	AU060328
C 18	10	76.9	55	13	B1946339	B1946339	sr87604.y
C 19	10	76.9	56	17	AZ363074	AZ363074	AZ363074
C 20	10	76.9	56	17	BH847572	BH847572	SALK_0547
C 21	10	76.9	57	12	BF643255	BF643255	NE004G01E
C 22	10	76.9	57	17	BH847577	BH847577	SALK_0547
C 23	10	76.9	58	14	B0567340	B0567340	g188d04.y
C 24	10	76.9	59	17	BH854923	BH854923	SALK_0872
C 25	10	76.9	63	9	A1949463	A1949463	wq10d10.x
C 26	10	76.9	65	17	BH813114	BH813114	SALK_0637
C 27	10	76.9	69	13	BM270723	BM270723	sak16q10.
C 28	10	76.9	69	17	BH857895	BH857895	SALK_0875
C 29	10	76.9	70	9	AU013546	AU013546	AU013546
C 30	10	76.9	70	9	AU013844	AU013844	AU013844
C 31	10	76.9	71	17	AZ833202	AZ833202	2M0115E08
C 32	10	76.9	72	13	B1943231	B1943231	so07a02.y
C 33	10	76.9	73	9	AA724688	AA724688	a113h09.s
C 34	10	76.9	74	17	AL768789	AL768789	Arabidops
C 35	10	76.9	75	14	N85300	N85300	J3129P.Huma
C 36	10	76.9	76	17	AZ853764	AZ853764	2M0157C10
C 37	10	76.9	78	10	AV957827	AV957827	HUMGS00884
C 38	10	76.9	78	14	D19926	D19926	HUMGS00884
C 39	10	76.9	80	9	AU010897	AU010897	AU010897
C 40	10	76.9	80	17	TA94H050	TA94H050	Al465459.T.brucel
C 41	10	76.9	81	17	BH853043	BH853043	SALK_0755
C 42	10	76.9	81	17	BH854995	BH854995	SALK_0870
C 43	10	76.9	81	17	BH857864	BH857864	SALK_0875
C 44	10	76.9	82	9	AU010817	AU010817	AU010817
C 45	10	76.9	82	9	AU010818	AU010818	AU010818

ALIGNMENTS

RESULT 1
AU258344
LOCUS
DEFINITION AU258344 3'-directed mouse cDNA library Mus musculus cDNA clone
AU258344
ACCESSION
VERSION AU258344.1 GI:20323820
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Generation of expressed sequence tags from mouse brain
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@bs.aist-nara.ac.jp
URL: http://love2.aist-nara.ac.jp/BBD/index.html.
1. 21
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BBD0012727"

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/clone_lib="3'-directed mouse cDNA library"
/class_type="brain"
/notes="Vector: pGEM-T-easy"
BASE COUNT      11 a      2 c      1 g      7 t
ORIGIN

Query Match      76.9%; Score 10; DB 9; Length 21;
Best Local Similarity 76.9%; Pred. NO. 3.5e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATCAANNANTTA 13
        ||||| 1 |||
Db      7 AATCAAAATTTTA 19

RESULT 2
BH854703/c      29 bp      DNA      linear      GSS 08-JUL-2002
LOCUS      BH854703
DEFINITION      Arabidopsis thaliana TDNA insertion lines
                Arabidopsis thaliana genomic clone SALK_088982.46.95.x, DNA
                sequence.
ACCESSION      BH854703
VERSION        BH854703.1
KEYWORDS       GSS.
SOURCE         thale cress.
ORGANISM       Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE      1 (bases 1 to 29)
AUTHORS        Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriah,
                C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
                Zimmerman,J., and Ecker,J.R.
                A Sequence-Indexed Library of Insertion Mutations in the
                Arabidopsis Genome
                Unpublished (2001)
                Contact: Joseph R. Ecker
                Salk Institute Genomic Analysis Laboratory (SIGAL)
                The Salk Institute for Biological Studies
                10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                Tel: 858 453 4100 x1752
                Fax: 858 558 6379
                Email: jecker@salk.edu
                This is single pass sequence recovered from the left border of
                TDNA. This sequence lies within 300 bases of the 5' end of
                A5953910.
                Class: TDNA tagged.
FEATURES
    source      Location/Qualifiers
                1..29
                /organism="Arabidopsis thaliana"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_088982.46.95.x"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/cdna_protocols.html"
BASE COUNT      11 a      1 c      4 g      13 t
ORIGIN

Query Match      76.9%; Score 10; DB 17; Length 29;
Best Local Similarity 76.9%; Pred. NO. 4e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATCAANNANTTA 13
        ||||| 1 |||
Db      15 AATCAAAATTTTA 3

RESULT 3

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```

A2837501/c      31 bp      DNA      linear      GSS 20-FEB-2001
LOCUS      A2837501
DEFINITION      2M0132M13R Mouse 10kb plasmid UUC1M library Mus musculus genomic
                clone UGCC2M0132M13 R, DNA sequence.
ACCESSION      A2837501
VERSION        A2837501.1
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 31)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamll,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
                M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                and Wright,D., Weiss,R.
                Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
                Unpublished (2000)
                Contact: Robert B. Weiss
                University of Utah Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0132 row: M column: 13
                Seq primer: CACACGAGAAACAGCTATGACC
                Class: plasmid sense
                High quality sequence stop: 31.
FEATURES
    source      Location/Qualifiers
                1..31
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGCC2M0132M13"
                /clone_lib="Mouse 10kb plasmid UUC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMDA2 (g1473211419b1A1F29072.1), a copy-number
                indelible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the Insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT      6 a      4 c      9 g      12 t
ORIGIN

Query Match      76.9%; Score 10; DB 17; Length 31;
Best Local Similarity 76.9%; Pred. NO. 4.2e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATCAANNANTTA 13
        ||||| 1 |||
Db      27 AATCAAAATTTTA 15

RESULT 4

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BH854706/c
LOCUS BH854706 34 bp DNA linear GSS 08-JUL-2002
DEFINITION SALK_088979.46.35.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_088979.46.35.x, DNA
sequence.
ACCESSION BH854706
VERSION BH854706.1 GI:21704296
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 34)
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
AUTHORS ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J., and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
TITLE Unpublished (2001)
JOURNAL Contact: Joseph R. Ecker
COMMENT The Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g53910.
Class: TDNA tagged.
FEATURES
source
location/Qualifiers
1..34
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_088979.46.35.x"
/note="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html
BASE COUNT 11 a 3 c 4 g 15 t 1 others
ORIGIN
Query Match 76.9%; Score 10; DB 17; Length 34;
Best Local Similarity 76.9%; Pred. No. 4.3e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
||||| |
DB 20 AATCAATATTTA 8
RESULT 5
AZ439152 35 bp DNA linear GSS 03-OCT-2000
LOCUS AZ439152
DEFINITION 1M0229G08R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0229G08 R, DNA sequence.
ACCESSION AZ439152
VERSION AZ439152.1 GI:10563165
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: G column: 08
Seq primer: CACACAGCAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
source
location/Qualifiers
1..35
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0229G08"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.
BASE COUNT 13 a 8 c 0 g 14 t
ORIGIN
Query Match 76.9%; Score 10; DB 17; Length 35;
Best Local Similarity 76.9%; Pred. No. 4.4e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATCAANNANTTA 13
||||| |
DB 6 AATCAATCATTTTA 18
RESULT 6
BH854728/c 36 bp DNA linear GSS 08-JUL-2002
LOCUS BH854728
DEFINITION SALK_088935.40.95.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_088935.40.95.x, DNA
sequence.
ACCESSION BH854728
VERSION BH854728.1 GI:21704318
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 36)
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
AUTHORS ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

TITLE Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute for Biological Studies (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
AT5g53910.
Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..36
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_088935.40.95.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 12 a 3 c 5 g 16 t

ORIGIN

Query Match 76.9%; Score 10; DB 17; Length 36;
Best Local Similarity 76.9%; Pred. NO. 4.4e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13
||||| |
Db 22 AATCAANNATTTA 10

RESULT 7
BH854701/c 37 bp DNA linear GSS 08-JUL-2002
LOCUS SALK_088987.31.80.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_088987.31.80.x, DNA
sequence.
ACCESSION BH854701
VERSION BH854701.1 GI:21704291
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 37)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute for Biological Studies (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
AT5g53910.
Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..37
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_087236.29.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 12 a 3 c 7 g 15 t

ORIGIN

Query Match 76.9%; Score 10; DB 17; Length 37;

source 1..37
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_088987.31.80.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 12 a 3 c 6 g 15 t

ORIGIN

Query Match 76.9%; Score 10; DB 17; Length 37;

RESULT 8
BH854911/c 37 bp DNA linear GSS 08-JUL-2002
LOCUS SALK_087236.29.60.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_087236.29.60.x, DNA
sequence.
ACCESSION BH854911
VERSION BH854911.1 GI:21704501
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 37)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute for Biological Studies (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
AT5g53910.
Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..37
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_087236.29.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 12 a 3 c 7 g 15 t

ORIGIN

Query Match 76.9%; Score 10; DB 17; Length 37;

Best Local Similarity 76.9%; Pred. No. 4.5e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13
|||||
DB 23 AATCAATTAATTTA 11

RESULT 9

AZ359655/c

LOCUS AZ359655 46 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0102A08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0102A08 R, DNA sequence.

ACCESSION AZ359655
VERSION AZ359655.1 GI:10473355

KEYWORDS

SOURCE GSS.

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 46)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: A column: 08
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers

FEATURES

source

1..46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0102A08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

9 a 5 c 7 g 25 t

Query Match

76.9%; Score 10; DB 17; Length 46;

Best Local Similarity 76.9%; Pred. No. 4.9e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATCAANNANTTA 13
|||||
DB 32 AATCAATGAATTA 20

RESULT 10

AZ508716/c

LOCUS AZ508716 46 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0351114F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0351114 F, DNA sequence.

ACCESSION AZ508716
VERSION AZ508716.1 GI:10690032

KEYWORDS

SOURCE GSS.

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 46)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0351 row: I column: 14
Seq primer: CGTTCGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers

FEATURES

source

1..46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0351114"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

17 a 7 c 5 g 17 t

Query Match

76.9%; Score 10; DB 17; Length 46;

Best Local Similarity 76.9%; Pred. No. 4.9e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
|||||
Db 41 AATCAAGCATTTA 29

RESULT 11

AZ481968/c

LOCUS 47 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0306110R Mouse 10kb plasmid UUGCJM library Mus musculus genomic
clone UUGCJM0306110 R, DNA sequence.

ACCESSION AZ481968
VERSION AZ481968.1 GI:10643033

KEYWORDS

SOURCE

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0306 row: 1 column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers

FEATURES

source

1. 47
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCJM0306110"
/clone_lib="Mouse 10kb plasmid UUGCJM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT

ORIGIN

12 a 3 c 7 g 25 t

Query Match

76.9%; Score 10; DB 17; Length 47;

Best Local Similarity 76.9%; Pred. No. 5e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
|||||
Db 29 AATCAAGCATTTA 17

RESULT 12

AV856952/c

LOCUS 49 bp mRNA linear EST 08-NOV-2001
DEFINITION AV856952 Nori Satoh unpublished cDNA library, larva Clona
intestinalis cDNA clone rcilv17a07 3', mRNA sequence.

ACCESSION AV856952
VERSION AV856952.1 GI:16844476

KEYWORDS

SOURCE

ORGANISM

Clona intestinalis.
Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Clona.
1 (bases 1 to 49)

REFERENCE Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scidlan.zool.kyoto-u.ac.jp.

JOURNAL

COMMENT

Location/Qualifiers
1. 49
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="rcilv17a07"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
/tissue_type="whole animal"
/dev_stage="larva"
/note="Vector: pBluescript SK"

BASE COUNT

ORIGIN

17 a 9 c 20 t
Query Match 76.9%; Score 10; DB 10; Length 49;
Best Local Similarity 76.9%; Pred. No. 5e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATCAANNANTTA 13
|||||
Db 23 AATCAAGCATTTA 11

RESULT 13

BH810378

LOCUS 49 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK_049225 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_049225, DNA sequence.

ACCESSION BH810378
VERSION BH810378.1 GI:20388196

KEYWORDS

SOURCE

ORGANISM

thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 49)

REFERENCE Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gaditnab,
C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednits, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker

JOURNAL

COMMENT

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At3g04140.
Class: TDNA tagged.

FEATURES

source

1.49
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_049225"
/note="PCR was performed on Arabidopsis thaliana lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 21 a 5 c 3 g 20 t

ORIGIN

Query Match 76.9%; Score 10; DB 17; Length 49;
Best Local Similarity 76.9%; Pred. No. 5e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNATTA 13
||||| |
Db 2 AATCAATACTTA 14

RESULT 14
BH861490/c 49 bp DNA linear GSS 05-AUG-2002
LOCUS SALK_081694 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_081694, DNA sequence.
ACCESSION BH861490
VERSION BH861490.1 GI:22096816
KEYWORDS CSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 49)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g3910.
Class: TDNA tagged.

FEATURES

source

1.49
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_081694"
/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 15 a 4 c 6 g 24 t

ORIGIN

Qy 1 AATCAANNATTA 13
||||| |
Db 35 AATCAATATTTA 23

RESULT 15
A0257483 51 bp mRNA linear EST 25-APR-2002
LOCUS A0257483 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0010659 3', mRNA sequence.
ACCESSION A0257483
VERSION A0257483.1 GI:20322147
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 51)
Kato,K. and Matoba,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatoids.aist-nara.ac.jp.
URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1.51
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0010659"
/clone_1b="3'-directed mouse cDNA library"
/tissue-type="brain"
/note="Vector: pGEM-T-easy"
BASE COUNT 18 a 9 c 17 t

Query Match 76.9%; Score 10; DB 9; Length 51;
Best Local Similarity 76.9%; Pred. No. 5.1e+04;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATCAANNATTA 13
||||| |
Db 20 AATCAGACTTA 32

Search completed: December 26, 2002, 14:02:52
Job time : 1979 secs

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